

OM protein - protein search, using sw model.
Run on: January 6, 2002, 09:47:04 ; Search time 22.43 Seconds
Copyright (c) 1993 - 2000 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

XX WPI; 1995-264505/35.

XX Antigen-specific activated T-lymphocytes and their detection - by
XX interaction with inventive peptide(s) of peptide-MHC complexes;
XX used in diagnosis of e.g. diabetes and auto-immune diseases.

XX PCT PCT PPS PPS PPS Sequence

XX Claim 1; Page 13; 21PP; German.

XX AR88667' is derived from residues 266-290 of human glutamic acid
XX decarboxylase and specifically reacts with a T-cell population
XX isolated from recently diagnosed Type-I diabetics. Pharmaceutical
XX compns. contg. this peptide and those shown in AR88668 and
XX AR76612-62, are useful for the diagnosis or predisposition
XX of immune system diseases, tumours, and autoimmune diseases, including
XX diabetes. The peptides are able to detect specific T-cell subpopulations
XX that are then used for antigen prodn., e.g. by reinjection.

XX 25 AA;

Query	Match	Score 100.0%	DB 16;	Length 25;
	Best Local Similarity	Pred. No. 8.5-15;		
	Matches 25; Conservative	0; Mismatches	Indels 0;	Gaps 0;
Qy	1 GMAALPRLIAATSENSHFSIKKGAA	25		
Ddb	1 qmaalprliaatsenhfsikkgaa	25		

AS	Synthetic.						
OS							
XX							
XX							
PN	DE19526561-A1.						
XX							
PD	23-JAN-1997.						
XX							
PF	20-JUL-1995;	95DBE-1026561.					
XX							
PF	20-JUL-1995;	95DBE-1026561.					
XX							
PR	PA	(BOEFL) BOEHRINGER MANNHEIM GMBH.					
XX							
PI	Donie F, Endl J, Ganz M,	Jung G,	Klientsch-engel R;				
PI	Pozzilli P,	Stahl P;					
XX							
DR	WPI; 1997-088254/09.						
XX							

PT involving intradermal admin. of auto:reactive substances
XX
XX
PS Claim 11: Page 10; 12pp; German.
XX

CC establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.

```

Query Match      100.0%;   Score 125; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 GMAALPRLIAFTSEHSHFLSKGAA 25
Db   1 gmaalprliaftsehshflskgaa 25

```

AAR72279 ID AAR72279 standard; Peptide: 20 AA.
 XX AC AAR72279;
 XX DT 13-NOV-1995 (first entry)
 XX DE Glutamic acid decarboxylase (GAD65
 XX

KW insulin-dependant diabetes mellitus; stiff man disease.
 XX OS Homo sapiens.
 XX PN WO9507992-A.
 XX PD 23-MAR-1995.
 XX PP 24-AUG-1994; 94WO-US09478.

ans
PR 17-SEP-1993; 93US-0123859.
XX
(RECC) UNIV CALIFORNIA.
PA

PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 XX WPI; 1995-131360/17.
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of auto-immune disease, esp. insulin
 PT related diseases, also related nucleic acid, vectors, :
 PT antibodies, hybridoma(s) etc.
 PT

PS Example 11: Page 76; 100PP; English.
 XX AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human
 CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD66
 CC fragments described in AAR7261-R72398 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependent diabetes mellitus or stiff man disease.
 CC
 CC
 CC
 CC

Query	Match	Score	DB	Length	Gaps
Qy	10	AFTSEHSHSISLKGAA	25	0	0
Db	1	aftsehshsikgaa	16	0	0

RESULT 4
 AAY59552 standard; peptide; 20 AA.
 XX
 AC AAY59552;
 XX
 DT 03-APR-2000 (first entry)
 XX
 DE GAD65 fragment, peptide #19.
 XX
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM; insulin dependant diabetes mellitus; Stiff man disease; diagnosis; therapy.
 KW Homo sapiens.
 XX
 PN US5998366-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 09-APR-1997; 97US-0827618.
 XX
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0580536.
 PR 18-JUN-1991; 91US-0716909.
 PA (REGC) UNIV CALIFORNIA.
 PI Tobin AJ, Kaufman DL, Erlander MG;
 XX
 DR WPI; 2000-09530/08.
 XX
 PT Ameliorating glutamic acid decarboxylase associated autoimmune disease - for disorders such as insulin dependant diabetes mellitus and Stiff man disease.
 XX
 PS Claim 1; Column 42; 61pp; English.
 XX
 CC This sequence represents a fragment of the glutamic acid decarboxylase 65 (GAD65) protein. The invention relates to a method of ameliorating GAD associated autoimmune disorders by administering a GAD65 peptide to the patient. The method can be used for ameliorating GAD associated autoimmune disorders such as IDDM (insulin dependant diabetes mellitus) and Stiff man disease. GAD65 can also be useful for screening drugs that alter GAD function, for generating monoclonal antibodies and in immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM and the diagnosis is quite easy. It is also possible to obtain much larger quantities of polypeptide via recombinant techniques than are available from natural sources.
 XX
 SQ Sequence 20 AA;

Query Match	Best Local Similarity	Score	DB	Length
Matches 14; Conservative	100.0%	67	16	20
	0	Mismatches	0	
	0	Indels	0	
	0	Gaps	0	

RESULT 6
 QY 1 GMALALPRLIAFUSE 14
 ID AAY59578 standard; peptide; 20 AA.
 DB 7 gmaalpliafuse 20

RESULT 6
 QY 1 GMALALPRLIAFUSE 14
 ID AAY59578 standard; peptide; 20 AA.
 DB 7 gmaalpliafuse 20

RESULT 6
 QY 1 GMALALPRLIAFUSE 14
 ID AAY59578 standard; peptide; 20 AA.
 DB 7 gmaalpliafuse 20

RESULT 6
 QY 1 GMALALPRLIAFUSE 14
 ID AAY59578 standard; peptide; 20 AA.
 DB 7 gmaalpliafuse 20

RESULT 6
 QY 1 GMALALPRLIAFUSE 14
 ID AAY59578 standard; peptide; 20 AA.
 DB 7 gmaalpliafuse 20

RESULT 5
 ID AAR72278 standard; peptide; 20 AA.
 XX
 AC AAR72278;
 XX
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;

KW	Insuulin-dependant diabetes mellitus; stiff man disease.
XX	OS Homo sapiens.
XX	PN W09507992-A.
XX	PD 23-MAR-1995.
XX	PF 24-AUG-1994; 94WO-US09478.
XX	PR 17-SEP-1993; 93US-0123859.
XX	PA (REGC) UNIV CALIFORNIA.
XX	PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
XX	DR WPI; 1995-131360/17.
PS	New polypeptide fragments of glutamic acid decarboxylase - for diagnosis and treatment of auto-immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridoma(s) etc.
XX	Example 11; Page 76; 100pp; English.
XX	AQ086481 and AQ086482 encode AAR7173 and AAR79105, rat and human glutamic acid decarboxylase (GAD65) respectively, from which the GAD65 fragments described in AAR72261-R72258 were derived. These fragments can be used to detect autoantibodies against GAD, e.g. to diagnose and treat GAD-related autoimmune disorders, such as insulin dependant diabetes mellitus or stiff man disease.
CC	Sequence 20 AA;
SQ	

XX antigen based immunotherapeutic agent, to a host afflicted with an autoimmune disease. The CC immunotherapeutic agent is used to treat autoimmune diseases such as CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory immune responses. The NNTA induces regulatory tolerance by elicitation of regulatory T cells among T cells recognizing the NNTA but CC not participating in the immune response. The NNTA are capable of CC recognition by substantial populations of uncommitted T cells which can CC be primed or biased, towards regulatory responses to provide effective CC treatment. The NNTA are effective in regulating undesirable immune CC responses even when target determinants used as agents promoting CC tolerance agents have failed to induce an effective regulatory T cell CC response. NNTAs as agents promoting tolerance are anticipated to be safer CC than use of target determinants.

PS Example 11; Column 42; 61PP; English.

XX This sequence represents a fragment of the glutamic acid decarboxylase 65 CC (GAD65) protein. The invention relates to a method of ameliorating GAD CC associated autoimmune disorders by administering a GAD65 Peptide to the CC patient. The method can be used for ameliorating GAD associated CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus) CC and Stiff man disease. GAD65 can also be useful for screening drugs that CC alter GAD function, for generating monoclonal antibodies and in CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM CC and the diagnosis is quite easy. It is also possible to obtain much CC larger quantities of polypeptide via recombinant techniques than are CC available from natural sources.

XX Sequence 20 AA;

Query Match Score 53.6%; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFSE 14
||| | | | | | | | | | | |
Db 7 gmaalprliafse 20

RESULT 7
ID AAY57065 standard; Peptide; 20 AA.
XX
AC AAY57065;
XX DT 28-FEB-2000 (first entry)
XX DE Glutamate decarboxylase peptide GAD p18.
XX Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
KW immunotherapeutic agent; insulin dependent diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
KW uveoretinitis; inflammatory response.
XX Homo sapiens.
XX WO956763-A1...
XX
PD 11-NOV-1999.
XX PF 07-MAY-1999; 99WO-US10250.
XX PR 07 MAY-1998; 98US-0084636.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Kaufman DL, Tian J, Olcott A;
XX DR WPI: 2000-052905/04.
XX PT Administration of neglected target tissue antigens to modulate immune
PT responses

PS Disclosure; Page 23; 79PP; English.

XX Amino acid sequences AAY57063-Y57091 are examples of neglected target
CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
CC not involved in autoimmunity. These peptides and proteins are used in
CC the method of the invention which involves administering an NNTA as an

CC antigen based immunotherapeutic agent, to a host afflicted with an autoimmune disease. The CC immunotherapeutic agent is used to treat autoimmune diseases such as CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory immune responses. The NNTA induces regulatory tolerance by elicitation of regulatory T cells among T cells recognizing the NNTA but CC not participating in the immune response. The NNTA are capable of CC recognition by substantial populations of uncommitted T cells which can CC be primed or biased, towards regulatory responses to provide effective CC treatment. The NNTA are effective in regulating undesirable immune CC responses even when target determinants used as agents promoting CC tolerance agents have failed to induce an effective regulatory T cell CC response. NNTAs as agents promoting tolerance are anticipated to be safer CC than use of target determinants.

PS Sequence 20 AA;

Query Match Score 51.2%; DB 21; Length 20;
Best Local Similarity 92.9%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFSE 14
||| | | | | | | | | | | |
Db 7 gmaalprliafse 20

RESULT 8
ID AAB07785 standard; peptide; 24 AA.
XX
AC AAB07785;
XX DT 07-NOV-2000 (first entry)
XX DE Glutamic acid decarboxylase-65 (GAD-65) analogue peptide.
XX KW Glutamic acid decarboxylase-65; GAD-65; autoimmune disease;
KW insulin-dependent diabetes mellitus; IDDM; stiff man syndrome;
KW cellular autoimmune response; T-cell receptor; autoimmune antigen.
XX Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 15
FT /label= Thr, Glu
XX EP1026238-A2.
XX PN 09-AUG-2000.
XX PD 09-AUG-2000.
XX PR 17-JUN-1992; 2000EP-0102229.
XX PR 18-JUN-1991; 91US-0716909.
PR 17-JUN-1992; 92EP-0110308.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Tobin AJ, Erlander MG, Kaufman DL, Clare-Salzler MJ;
XX DR WPI: 2000-500251/45.
XX Diagnosing and treating autoimmune diseases such as insulin-dependent diabetes mellitus and detecting antibodies to glutaminic acid decarboxylase (GAD65 in a sample, using GAD65 polypeptide -
XX Claim 15; Page 2; 32PP; English.

XX The specification describes a method which uses a glutamic acid CC decarboxylase-65 (GAD-65) polypeptide or analogue for diagnosing and CC treating autoimmune diseases such as insulin-dependent diabetes CC mellitus (IDDM). The polypeptide is useful for diagnosing IDDM and CC

AC AAJ03390;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3381.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PP 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Example 5; Page 198; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C Virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
 Best Local Similarity 61.5%; Pred. No. 8.7; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative 1; MisMatches 4; Indels 0; Gaps 0;
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
 Best Local Similarity 61.5%; Pred. No. 8.7; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative 1; MisMatches 4; Indels 0; Gaps 0;
 XX
 OY 7 RLIAFTSEHSHS 19
 DB 3 rliafasrgnhs 15

RESULT 15
 AAJ04073
 ID AAJ04073 standard; Peptide: 15 AA.
 XX
 AC AAJ04073;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #4064.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PP 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Example 5; Page 201; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
 Best Local Similarity 61.5%; Pred. No. 8.7; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative 1; MisMatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFTEHSHFS 19
| | | | | : | |
DB 3 rliafaargnvs 15

RESULT 16
AAW01981
ID AAW01981; standard; peptide; 20 AA.
XX
AC AAW01981;
XX
DT 26-SEP-1996 (first entry)
DE Antigenic peptide comprising HCV NS4 protein residues 1916-1935.
XX
KW Antigenic peptide; C-terminal region; hepatitis C virus; HCV;
KW non-A non-B; non-structural protein 4; NS4; differential diagnosis;
KW acute; chronic; infection; binding assay.
XX
OS Hepatitis C virus.
XX
PN WO9604300-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-US09599.
XX
PR 29-JUL-1994; 94US-0282758.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI: 1996-129330/13.
XX
PT Antigenic peptide(s) binding anti-hepatitis C virus antibodies
PT useful for differential diagnosis of HCV in subjects
XX
PS Claim 3; Page 27; 50pp; English.

CC The present peptide is an antigenic peptide (AP), derived from the C-terminal region of the hepatitis C virus (HCV) non-structural protein 4 (NS4). The AP was prepared, using Fmoc chemistry, and can be used in a claimed method for the differential diagnosis of HCV. One, two or three of the peptides AAW01980-82 are separately contacted with an antibody (Ab) contg. sample, and the binding between the peptide(s) and the Ab determined. The Ab contg. sample is then contacted with the peptide AAW01983, and the binding between the peptide and the Ab determined. The strength of the binding between the peptide(s) and the Ab in the two assays is compared, where stronger binding in the 1st assay is indicative of acute HCV infection, and equivalent binding is indicative of chronic HCV infection.
XX
SQ Sequence 20 AA;

XX 28-FEB-2000 (first entry)
DT Hepatitis C virus (HCV)-derived MHC class II (HTL) epitope, #251.
XX
DE Chimeric; pan DR epitope; expression vector; MHC; targeting peptide; promoter; major histocompatibility complex; MHC; targeting peptide; epitope; antigen; presentation; Class I; cytosolic pathway;
KW endoplasmic reticulum; class II; extracellular antigen; endocytic pathway; helper T lymphocyte; HTL; universal epitope;
KW cytotoxic lymphocyte; CTL; immune response; immunogenicity; assay; vaccine; immunity; infection; pathogen; virus; HRV; HBV; HCV;
KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell; autoimmune disease; activation; antiviral; antimalarial; immunoprotective.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO9586558-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10646.
XX
PR 13-MAY-1998; 98US-0078904.
XX
PR 15-MAY-1998; 98US-0085751.
XX
(EPIM-) EPIMUNE INC.
XX
Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
PI PI Chesnut RW;
XX
DR WPI: 2000-039103/03.
XX
PT Expression vectors encoding major histocompatibility targeting sequence, used as, e.g. tumor vaccines -
XX
PS Claim 11; Page 67; 130pp; English.
XX
CC Sequences AAY73087-Y73102 represent hepatitis C virus (HCV)-derived MHC class II (HTL) epitopes which are claimed for use in the present invention. The invention relates to a novel expression vector comprising a promoter operably linked to a fusion gene encoding a major histocompatibility complex (MHC) targeting sequence, and two or more heterologous peptide epitopes. The MHC targeting sequence may be a class I targeting sequence, which directs an MHC class I epitope to a cytosolic pathway or to the endoplasmic reticulum, or an MHC class II targeting sequence, which directs extracellular antigens to enter the endocytic pathway to be processed into antigen peptides for presentation on MHC class II molecules. The heterologous epitopes may comprise either helper T lymphocyte (HTL) epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL epitope such as a pan DR epitope (PADRE). The vectors are useful for stimulating an immune response *in vivo*, as well as for use in assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in a non-human mammal. They provide a nucleic acid vaccine for enhancing immunity against infectious pathogens, such as viruses (e.g., HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g., Plasmodium falciparum, the cause of malaria) and also tumour cells and autoimmune diseases. Universal MHC class II epitopes are advantageously combined with other MHC class I and class II epitopes to increase the number of cells that are activated in response to a given antigen and provide a broader population coverage of MHC-reactive alleles.
XX
SQ Sequence 22 AA;

Query Match 29.6%; Score 37; DB 17; Length 20;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFTEHSHFS 19
| | | | | : | |
DB 3 rliafaargnvs 15

RESULT 17
AAW73093
ID AAW73093 standard; Peptide; 22 AA.
XX
AC AAW73093;

Query Match 29.6%; Score 37; DB 21; Length 22;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFTEHSHFS 19

Db ||||| :| | 10 rliafasrgnvhvs 22

XX PF 16-SEP-1992; 92WO-US07865.

XX PR 16-SEP-1991; 91US-0762135.

PR 12-FEB-1992; 92US-0835717.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Burk KH, Dreesman GR, Pauletti D;

XX DR WPI; 1993-11737/14.

XX PT Detection of hepatitis C virus antigens - using HCV reactive antibody bound to solid support and competitive HCV antigen-reporter complex

XX PS Claim 27; Page 122; 190pp; English.

XX CC The synthetic peptide corresponds to residues 1917-1940 of the NS4 domain of HCV. The peptide may be used for the sensitive and specific detection of HCV infection. Antibodies raised against the peptide can be used for passive immuno-prophylaxis and the HCV antigens can be used in vaccines to prevent HCV infection.

CC See also AAR34041-65.

XX SQ Sequence 24 AA;

Query Match 29.6%; Score 37; DB 14; Length 24;

Best Local Similarity 61.5%; Pred. No. 15; Mismatches 8; Conservative 1; Indels 4; Gaps 0;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RIAFTSEHHSRS 19

DB 2 rliafasrgnvhvs 14

RESULT 20

AY41898 ID AY41898 standard; Peptide; 19 AA.

XX AC AY41898;

XX DT 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #49.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; XX rheumatoid arthritis diagnostic protein isoform; screening; XX expression reference protein isoform; prognosis.

OS Homo sapiens.

XX PN WO9947925-A2.

XX PD 23-SEP-1999.

XX PR 15-MAR-1999; 99WO-GB00763.

XX PR 13-MAR-1998; 98GB-0005477.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Parkh RB, Patel TP, Townsend RR;

XX DR WPI; 1999-571871/48.

XX PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis

XX Disclosure; Page 18; 157pp; English.

PS WO9306888-A.

XX OS Synthetic.

XX PN 01-APR-1993.

RESULT 19

AAR34043 ID AAR34043 standard; Peptide; 24 AA.

XX AC AAR34043;

XX DT 22-JUL-1993 (first entry)

XX DE HCV NS peptide DP3.

XX KW Hepatitis C virus; non structural region; antigen; diagnosis; vaccine.

XX OS Synthetic.

XX PN WO9306888-A.

XX PD 01-APR-1993.

CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of each chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY4184 to AAU42100 represent RP1 peptides, AAU42101 to AAU42103 represent expression reference protein isoform peptides and AAU25066 to AAU25068 represent degenerate probes for RPIS, which are all used in the exemplification of the present invention.

XX Sequence 19 AA;

Query Match 28.0%; Score 35; DB 20; Length 19;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 8 LIAFTSEHSHFLKKG 23
||: :||: |: |
DB 1 lisvdtdhsnlylqng 16

RESULT 21
AAU02448 standard; Peptide; 11 AA.
ID AAU02448;
AC AAU02448;
DT 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #2439.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX Hepatitis C virus.
XX Hepatitis C virus epitope #2439.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX Hepatitis C virus.
PN WO200121189-A1.
XX WPI; 2001-308046/32.
PR 19-JUL-1999; 99US-0357737.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX Disclosure: Page 169; 214pp; English.
PS The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAU0010-AAU04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX SQ Sequence 11 AA;

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 7 RLIAFTSEHSH 17
|: ||: |:
DB 1 rliafasrgnh 11

RESULT 23
AAW85304
ID AAW85304 standard; peptide; 21 AA.
AC AAW85304;
XX WPI; 2001-308046/32.
PR 19-JUL-1999; 99US-0357737.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX Disclosure: Page 160; 214pp; English.
PS The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAU0010-AAU04121.
CC These are derived from HCV HLA-binding motifs. They are useful in

CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX SQ Sequence 11 AA;

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SQ Sequence 11 AA;

RESULT 22
AAU02837
ID AAU02837 standard; Peptide; 11 AA.
AC AAU02837;

DT 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #2828.

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 7 RLIAFTSEHSH 17
|: ||: |:
DB 1 rliafasrgnh 11

RESULT 23
AAW85304
ID AAW85304 standard; peptide; 21 AA.
AC AAW85304;

DT 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #2828.

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 7 RLIAFTSEHSH 17
|: ||: |:
DB 1 rliafasrgnh 11

RESULT 23
AAW85304
ID AAW85304 standard; peptide; 21 AA.
AC AAW85304;

DT 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #2828.

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 7 RLIAFTSEHSH 17
|: ||: |:
DB 1 rliafasrgnh 11

RESULT 23
AAW85304
ID AAW85304 standard; peptide; 21 AA.
AC AAW85304;

DT 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #2828.

DT DT
 XX XX
 DE Helper T-cell class II peptide derived from NS4 protein.
 XX KW
 Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DRL;
 KW DR7; cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
 KW acquired immune deficiency syndrome; malaria; cancer;
 KW allograft rejection; allergy; Lyme disease; hepatitis;
 KW post-streptococcal endocarditis; glomerulonephritis;
 KW food hypersensitivity.

XX OS Synthetic C virus.
 OS Hepatitis C virus.
 XX WO9832456-A1.
 PN XX
 PD 30-JUL-1998.
 XX PF 23-JAN-1998; 98WO-US01373.
 XX PR 07-FEB-1997; 97US-0037432.
 PR 23-JAN-1997; 97US-0036713.

PA (EPIIM-) EPIMMUNE INC.
 XX PI Sette A., Sidney J., Southwood S;
 PT XX
 DR WPI; 1998-427679/36.

PS Disclosure: Page 40; 51pp; English.

XX AW85284-451 represent helper T-cell class II peptides, which can bind to the human leucocyte antigens (HLA) DR4w4, DRL and DR7. The peptides are used in the course of the invention. The specification describes peptides that that induce a cytotoxic T lymphocyte (CTL) response and T-helper peptides, that are used together to generate a CTL response for the treatment or prevention of viral, fungal, bacterial or parasitic infections (e.g. hepatitis, acquired immune deficiency syndrome or malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate cancer or condyloma acuminatum). Helper T-cell peptides may be used alone to induce a helper T cell response, e.g. in cases of autoimmune disease, allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal endocarditis, glomerulonephritis and food hypersensitivity.

XX Sequence 21 AA;

Query Match 27.2%; Score 34; DB 19; Length 21;
 Best Local Similarity 63.6%; Pred. No. 43; Mismatches 7; Conservative 1; Indels 0; Gaps 0;

QY ||||| | :| 7 RLIATFSESH 17
 Db 10 rliafasrgnh 20

RESULT 24
 AAV73094 standard; Peptide: 21 AA.
 ID AAV73094
 XX AC
 XX AAY73094;
 DT 28-FEB-2000 (first entry)
 XX DE Hepatitis C virus (HCV)-derived MHC class II (HHL) epitope, #252.
 KW XX Chimeric; pan DR epitope; expression vector;

OS Synthetic C virus.
 XX WO958658-A2.
 PN XX
 PD 18-NOV-1999.
 XX PF 13-MAY-1999; 99WO-US10646.
 XX PR 13-MAY-1998; 98US-0078904.
 XX PR 15-MAY-1998; 98US-0085751.

PA (EPIIM-) EPIMMUNE INC.
 XX PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 PT Chestnut RW;
 DR XX
 WPI; 2000-039103/03.

PS Claim 11; Page 67; 130pp; English.

PT Expression vectors encoding major histocompatibility targeting sequence, used as, e.g. tumor vaccines -
 XX PS

XX CC Sequences AAY73087-Y73102 represent hepatitis C virus (HCV)-derived MHC class II (HHL) epitopes which are claimed for use in the present invention. The invention relates to a novel expression vector comprising a promoter operably linked to a fusion gene encoding a major histocompatibility complex (MHC) targetting sequence, and two or more heterologous peptide epitopes. The MHC targetting sequence may be a class I targetting sequence, which directs an MHC class I epitope to a cytosolic pathway, or to the endoplasmic reticulum, or an MHC class II targetting sequence, which directs extracellular antigens to enter the endocytic pathway to be processed into antigen peptides for presentation on MHC class II molecules. The heterologous epitopes may comprise either helper T lymphocyte (HTL) epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HHL epitope such as a pan DR epitope (PADRE). The vectors are useful for stimulating an immune response *in vivo*, as well as for use in assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in non-human mammal. They provide a nucleic acid vaccine for enhancing immunity against infectious pathogens, such as viruses (e.g., HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g., Plasmodium falciparum, the cause of malaria) and also tumour cells and autoimmune diseases. Universal MHC class II epitopes are advantageously combined with other MHC class I and class II epitopes to increase the number of cells that are activated in response to a given antigen and provide a broader population coverage of MHC-reactive alleles.

XX SQ Sequence 21 AA;

Query Match 27.2%; Score 34; DB 21; Length 21;
 Best Local Similarity 63.6%; Pred. No. 43; Mismatches 7; Conservative 1; Indels 0; Gaps 0;

QY ||||| | :| 7 RLIATFSESH 17
 Db 10 rliafasrgnh 20

RESULT 25
 AAB82059

ID AAB82059 standard; peptide; 21 AA.
 XX
 AC AAB82059;
 XX
 AC
 XX DT 22-JUN-2001 (first entry)
 XX DE HCV antigen, NS4 1909-1929.
 XX KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
 XX KW viral infection.
 XX OS Hepatitis c virus.
 XX PN WO200124822-A2.
 XX PD 12-APR-2001.
 XX PP 02-OCT-2000; 2000WO-EP09657.
 XX PR 01-OCT-1998; 99AT-0001680.
 XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX PI Fleitmann J, Mattner F, Buschle M, Meiling J;
 XX DR WPI; 2001-290577/30.
 XX PT New pharmaceutical composition comprising an antigen, an immunostimulating substance and a polycationic polymer, useful in manufacturing vaccines
 PT
 XX PS Claim 12; Page 16; 20pp; English.
 XX CC The present invention relates to a pharmaceutical composition comprising an antigen; (b) an immunostimulating substance consisting of neuroactive compounds, hormones, compounds having growth hormone activity or their mixtures; and (c) a polycationic polymer. The present sequence is an antigenic peptide derived from Hepatitis C virus, which was used in the present invention. The composition is useful in manufacturing vaccines.
 XX SQ Sequence 21 AA;

Query Match 27.2%; Score 34; DB 22; Length 21;
 Best Local Similarity 63.6%; Pred. No. 43;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 7 RLIATSEHSH 17
 Db 10 rliafasrqnh 20

Search completed: January 6, 2002, 09:51:45
 Job time: 281 sec

RESULT 2

Query Match Score: 65.68; DB: 2; Length: 20;
 Best Local Similarity: 100.0%; Pred. No.: 7.4e-08;
 Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Appl. No.: 599366 Application US/08827618A
 Title of Invention: Cloned Glutamic Acid Decarboxylase
 Number of Sequences: 60
 Correspondence Address:
 Addressee: Flehr, Rohbach, Test, Albritton & Herbert
 Street: Four Embarcadero Center, Suite 3400
 City: San Francisco
 State: CA
 Country: US
 Zip: 94111-4187

Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentin Release #1.0, Version #1.30
 Current Application Data:
 Application Number: US/08/483,952A
 Filing Date: 07-JUN-1995
 Classification: 536
 Prior Application Data:
 Application Number: US 08/123,859
 Filing Date: 17-SEP-1993
 Classification: 536
 Prior Application Data:
 Application Number: US 07/716,909
 Filing Date: 18-JUN-1991
 Classification: 536
 Prior Application Data:
 Application Number: US 07/586,536
 Filing Date: 21-SEP-1990
 Classification: 536
 Attorney/Agent Information:
 Name: Trecartin, Richard F.
 Registration Number: 31,801
 Reference/Doctet Number: A-60780-7/RFT/MTK
 Telecommunication Information:
 Telephone: 415-781-1989
 Telefax: 415-398-3249
 Information for Seq ID No.: 32:
 Sequence Characteristics:
 Length: 20 amino acids
 Strandedness: single
 Topology: linear
 Molecule Type: peptide
 US-08-483-952A-32

Query Match Score: 65.68; DB: 3; Length: 20;
 Best Local Similarity: 100.0%; Pred. No.: 7.4e-08;
 Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Appl. No.: 599366 Application US/08827618A
 Title of Invention: Cloned Glutamic Acid Decarboxylase
 Number of Sequences: 60
 Correspondence Address:
 Addressee: Flehr, Rohbach, Test, Albritton & Herbert
 Street: Four Embarcadero Center, Suite 3400
 City: San Francisco

RESULT 3

Query Match Score: 65.68; DB: 2; Length: 20;
 Best Local Similarity: 100.0%; Pred. No.: 7.4e-08;
 Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Appl. No.: 6011139 Application US/08483952A
 General Information:

LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-483-952A-31

Query Match 53.6%; Score 67; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 GMAALPRLAFTSE 14
 Db 7 GMAALPRLAFTSE 20

RESULT 7
 US-08-159-339A-933
 ; Sequence 933, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Celis, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and their
 ; TITLE OF INVENTION: Uses
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-5834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-005030US
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELLEX:
 INFORMATION FOR SEQ ID NO: 933:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-159-339A-933

Qy 12 TSEHSHFSLK 21
 Db 1 TSEQHSYISK 10

RESULT 8
 5475086-14
 ; Patent No. 5475086
 ; APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN, DANIEL L.; CLARE-SALZLER, MICHAEL J.
 ; TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
 ; PEPTIDES
 ; NUMBER OF SEQUENCES: 14
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/135,849
 ; FILING DATE: 13-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 716,909
 ; FILING DATE: 18-JUN-1991
 ; APPLICATION NUMBER: 586,536
 ; FILING DATE: 21-SEP-1990
 ; SEQ ID NO:14:
 ; LENGTH: 8
 5475086-14

RESULT 9
 US-08-485-718-2
 ; Sequence 2, Application US/08485718
 ; Patent No. 5705626
 ; GENERAL INFORMATION:
 ; APPLICANT: Tobin, Allan J.
 ; APPLICANT: Erlander, Mark G.
 ; APPLICANT: Kaufman, Daniel L.
 ; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Rohnbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,718
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A60780-6/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3449
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 amino acids
 ; TYPE: amino acid

RESULT 10
 Query Match 31.2%; Score 39; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMALPRL 8
 |||||||
 Db 17 GMALPRL 24

RESULT 10
 Sequence 2, Application US/08484530
 Patent No. 5846740
 GENERAL INFORMATION:
 APPLICANT: Tobin, Allan J
 APPLICANT: Erlander, Mark G
 APPLICANT: Kaufman, Daniel L.
 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/827,618A
 FILING DATE: 09-APR-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,725
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-484-530-2

RESULT 12
 Query Match 31.2%; Score 39; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMALPRL 8
 |||||||
 Db 17 GMALPRL 24

RESULT 12
 Sequence 2, Application US/08483952A
 Patent No. 6011139
 GENERAL INFORMATION:
 APPLICANT: Tobin, Allan J
 APPLICANT: Erlander, Mark G
 APPLICANT: Kaufman, Daniel L.
 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111-4187
 COMPUTER READABLE FORM:

RESULT 11
 Query Match 31.2%; Score 39; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMALPRL 8
 |||||||
 Db 17 GMALPRL 24

RESULT 11
 US-08-827-618A-2
 ; Sequence 2, Application US/08827618A
 ; Patent No. 5998366
 ; GENERAL INFORMATION:
 ; APPLICANT: Tobin, Allan J

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,952A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,859
 FILING DATE: 17-SEP-1993
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/716,909
 FILING DATE: 18-JUN-1991
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
 TELEPHONE: 415-751-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-483-952A-2

Query Match 31.2%; Score 39; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GMAALPRL 8
 Db 17 GMAALPRL 24

RESULT 13
 US-08-282-758B-2
 Sequence 2, Application US/08282758B
 ; Patent No. 5670310
 GENERAL INFORMATION:
 APPLICANT: Fields, Howard A.
 APPLICANT: Khudyakov, Yury E.
 TITLE OF INVENTION: Methods and Compositions for
 Differential Diagnosis of Chronic and Acute Hepatitis C
 TITLE OF INVENTION: Virus Infection
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 ZIP: 30303
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/282,758B
 FILING DATE: 29-JUN-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Green, Jamie L.
 REGISTRATION NUMBER: 32,467
 REFERENCE/DOCKET NUMBER: 03063-0100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3700
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-282-758B-2

Query Match 29.6%; Score 37; DB 1; Length 20;
 Best Local Similarity 61.5%; Pred. No. 4.6;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 14
 PCT-US92-07865-3
 Sequence 3, Application PC/TUSS9207865
 GENERAL INFORMATION:
 APPLICANT: Dreesman, Gordon R.
 APPLICANT: Burk, Kenneth H.
 APPLICANT: Pauletti, Daniel
 TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Peter Dehliner
 STREET: 350 Cambridge Avenue, Suite 300
 CITY: Palo Alto
 STATE: CA
 COUNTY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/07865
 FILING DATE: 19920916

CLASSIFICATION:
 FILING DATE: 16-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 1600-0086.41
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: AMINO ACID
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus
 INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
 PCT-US92-07865-3

RESULT 15
 Query Match 29.6%; Score 37; DB 5; Length 24;
 Best Local Similarity 61.5%; Pred. No. 5.8; 1; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative

QY 7 RLIAFASRSHES 19
 ||||| :| |
 2 RLIAFASRGNHVS 14

RESULT 15
 US-08-159-339A-915

Sequence 915, Application US/08159339A
 Patent No. 6037135;

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and Their

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-159-339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

FAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1031:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-339A-1031

RESULT 17
 Query Match 28.0%; Score 35; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05; 1; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative

TELE:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 915:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-159-339A-915

RESULT 17

Query Match 28.0%; Score 35; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05; 1; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative

TELE:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 915:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-159-339A-915

Query Match 28.0%; Score 35; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05; 1; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative

TELE:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 915:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-159-339A-915

APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Ellis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-0050300US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 978:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-159-339A-978

RESULT 18
 Query Match 27.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred No. 1.6e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;
 Db 1 VLFTEQQH 9

APPLICANT:
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES AND THEIR IMMUNOLOGICALLY IMPORTANT EPITOSES AND THEIR CORRESPONDING ANTI-BODIES OR BIOTINYLATED PEPTIDES
 TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTI-BODIES OR BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOSES,
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOSES,
 NUMBER OF SEQUENCES: 453
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/723,425A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 14,87-13
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4100
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: HCV
 FEATURE:

NAME/KEY: Modified-site
 LOCATION: 1
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 22
 US-08-723-425A-58

Query Match 27.2%; Score 34; DB 4; Length 22;
 Best Local Similarity 63.6%; Pred. No. 17; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIATFSEHSH 17
 ||||| :|
 Db 11 RLIAFASRGHN 21

RESULT 20

US-09-112-206-58
 Sequence 58; Application US/09112206
 Patent No. 611093

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
 TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE AND THEIR
 TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE,
 TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM,
 NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,718

FILING DATE: 07-JUN-1995

CLASSIFICATION: 536.

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-6/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-338-3249

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-485-718-1

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-484-530-1

Query Match 26.4%; Score 33; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 27; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

ZIP: 94111-1187

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,530

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-6/BIR

US-08-485-718-1

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-484-530-1

Query Match 26.4%; Score 33; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 27; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

ZIP: 94111-1187

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,530

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-6/BIR

US-08-484-530-1

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-484-530-1

Query Match 26.4%; Score 33; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 27; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

ZIP: 94111-1187

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,530

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-6/BIR

US-08-484-530-1

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-484-530-1

Query Match 26.4%; Score 33; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 27; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

ZIP: 94111-1187

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,530

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-6/BIR

US-08-484-530-1

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-484-530-1

Query Match 26.4%; Score 33; DB 1; Length 23;

Best Local Similarity 75.0%; Pred. No. 27; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

ZIP: 94111-1187

NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-484-530-1

Query Match 26.4%; Score 33; DB 2; Length 23;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GMAALPRL 8
 Db 16 GMAAVPKL 23

RESULT 23
 US-08-827-618A-1
 / Sequence 1, Application US/08827618A
 / Patent No. 5998366
 / GENERAL INFORMATION:
 / APPLICANT: Tobin, Allan J
 / APPLICANT: Eriander, Mark G
 / APPLICANT: Kaufman, Daniel L.
 / TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 / NUMBER OF SEQUENCES: 60
 / CURRENT APPLICATION DATA:
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 / STREET: Four Embarcadero Center, Suite 3400
 / CITY: San Francisco
 / STATE: CA
 / COUNTRY: US
 / ZIP: 94111-4187
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/827,618A
 / FILING DATE: 09-APR-1997
 / CLASSIFICATION: 435
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/485,725
 / FILING DATE: 07-JUN-1995
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/586,536
 / FILING DATE: 18-JUN-1991

PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/716,909
 / FILING DATE: 21-SEP-1990
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Trecartin, Richard F.
 / REGISTRATION NUMBER: 31,801
 / TELECOMMUNICATION INFORMATION:
 / NAME: Trecartin, Richard F.
 / REGISTRATION NUMBER: 31,801
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-781-1989
 / TELEFAX: 415-398-3249
 / INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 23 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-483-952A-1

Query Match 26.4%; Score 33; DB 3; Length 23;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GMAALPRL 8

RESULT 24
 US-08-483-952A-1
 / Sequence 1, Application US/08483952A
 / Patent No. 6011139
 / GENERAL INFORMATION:
 / APPLICANT: Tobin, Allan J
 / APPLICANT: Eriander, Mark G
 / APPLICANT: Kaufman, Daniel L.
 / TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 / NUMBER OF SEQUENCES: 60
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 / STREET: Four Embarcadero Center, Suite 3400
 / CITY: San Francisco
 / STATE: CA
 / COUNTRY: US
 / ZIP: 94111-4187
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/483,952A
 / FILING DATE: 07-JUN-1995
 / CLASSIFICATION: 536
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/123,859
 / FILING DATE: 17-SEP-1993
 / CLASSIFICATION: 536
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/586,536
 / FILING DATE: 21-SEP-1990
 / CLASSIFICATION: 536
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Trecartin, Richard F.
 / REGISTRATION NUMBER: 31,801
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-781-1989
 / TELEFAX: 415-398-3249
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 23 amino acids
 / TOPOLGY: linear
 / MOLECULE TYPE: peptide
 US-08-483-952A-1

Query Match 26.4%; Score 33; DB 3; Length 23;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GMAALPRL 8

Db ||||:||
16 GMAAVPKL 23

RESULT 25
5475086-8
;PATENT NO. 5475086
;APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN,
;DANIEL L.; CLARE-SALZLER, MICHAEL J.
;TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
;PEPTIDES
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/135,849
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 716,909
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 586,536
FILING DATE: 21-SEP-1990
SEQ ID NO:8;
LENGTH: 24
5475086-8

Query Match 26.4%; Score 33; DB 6; Length 24;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAAVPKL 8
Db ||||:||
17 GMAAVPKL 24

Search completed: January 6, 2002, 09:52:30
Job time: 226 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: January 6, 2002, 09:49:29 ; Search time 19.62 Seconds

(without alignments)
97.062 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 125

Sequence: 1 GMALPRLAIFTSEHSHFSLIKKGAA 25

Scoring table: BLOSUM62

GaPop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:
4959

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	32	25.6	25	2	H64710		hypothetical protein HP1528 - Helicobacter pylori (strain 26695)
2	29	23.2	20	2	S03954		hypothetical protein
3	27	21.6	14	2	P50249		acidic fibroblast
4	26	20.8	10	2	PC2171		porin - rice (stra
5	26	20.8	22	2	B39138		tracylglycerol li
6	26	20.8	24	2	T73619		dihydrofolipamide S
7	25	20.0	8	2	XGUEU		endothelial growth
8	25	20.0	22	2	A28563		urine glycopeptide
9	24.5	19.6	20	2	S07232		hemoglobin chain I
10	24	19.2	20	2	A53875		ribulose-bisphosph
11	24	19.2	22	2	S40638		creatine kinase (E
12	24	19.2	22	2	F84018		ATP-43 protein - h
13	24	19.2	25	2	J00361		hypothetical prote
14	23	18.4	14	2	A60770		vasoactive intesti
15	23	18.4	15	2	PS0455		cell surface alioa
16	23	18.4	15	2	PT0094		superoxide dismuta
17	23	18.4	18	2	S6627		succinate dehydro
18	23	18.4	22	2	A17267		tau protein - huma
19	23	18.4	22	2	PH6433		complement C4 - gu
20	23	18.4	23	2	A36912		protein T17H7.9 l1
21	23	18.4	24	2	S09363		Maud protein - Par
22	23	18.4	24	4	S03954		hypothetical prote
23	22	17.6	10	2	S74176		hypothetical McCol
24	22	17.6	12	2	S01122		glucuronidase (EC
25	22	17.6	12	2	PH1630		photosystem II 3.7
26	22	17.6	13	2	B61620		Ig H chain V-D-J R
27	22	17.6	15	2	PA007		IgG1 antibody
28	22	17.6	16	2	A85827		cytochrome c2 - fu
29	17.6	16	18	2	S48862		his operon leader

ALIGNMENTS

30	22	17.6	19	2	S43652		serpin WSZCI - whe
31	22	17.6	20	2	B41299		T-cell receptor al
32	22	17.6	20	2	A85645		Amino terminal of
33	22	17.6	22	2	S59071		secretory protein
34	22	17.6	22	2	I37144		aspartylglycosamin
35	22	17.6	23	2	S51188		aldehyde dehydro
36	22	17.6	25	2	S36358		isocitrate dehydro
37	22	17.6	21	2	I49414		Ig heavy chain V
38	21.5	17.2	23	2	PH1641		gene CTI4-1-prote
39	21.5	17.2	23	4	A35039		Ig H chain V-D-J R
40	21	16.8	6	4	A38929		hypothetical colla
41	21	16.8	13	2	R56046		glutathione peroxi
42	21	16.8	13	1	I4F6CH		urinary tract ston
43	21	16.8	16	2	C39509		his operon leader
44	21	16.8	16	2	C61414		mannose-specific 1
45	21	16.8	16	2	S59717		chymotrypsin (EC 3
46	21	16.8	17	2	B42408		21K high mobility
47	21	16.8	18	2	B42408		hypothetical prote
48	21	16.8	19	2	S59717		ribosomal protein
49	21	16.8	20	2	S78760		hypothetical prote
50	21	16.8	22	2	PT0070		

Best Local Similarity 35.7%; Pred. No. 3e+02; 3; Mismatches 6; Indels 0; Gaps 0;

Qy 5 LPRLI AFTSEHSHF 18
| | : | |
Db 3 LPPKLYSSNGHF 16

RESULT 3
porin - rice' (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0249
R;Tsugita, A.
submitted to JIBID, April 1993
A;Reference number: PS0206
A;Accession: PS0249
A;Molecule type: Protein
A;Residues: 1-14 <RSD>
A;Experimental source: callus

Query Match Score 27; DB 2; Length 14;
Best Local Similarity 30.8%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 9 IAFTSEHSHFSTIK 21
: | | : | : |
Db 2 VTFDDHTANGIK 14

RESULT 4
PC2171 triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragment)
C;Species: Rhizopus niveus
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171
R;Kohno, M.; Kugimura, W.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
A;Title: Purification, characterization, and crystallization of two types of lipase from
A;Reference number: PC2171; MUID:94319059
A;Accession: PC2171
A;Molecule type: protein
A;Residues: 1-10 <KOH>
C;Comment: this enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase

Query Match Score 26; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AALPRLIA 10
| | | | | : |
Db 3 AALPLLIS 10

RESULT 5
B39138 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Pelobacter carbinolicus (fragment)
C;Species: Pelobacter carbinolicus
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 05-May-2000
C;Accession: B39138
R;Oppermann, F.B.; Schmidt, B.; Steinbüchel, A.
J. Bacteriol. 173, 757-767, 1991
A;Title: Purification and characterization of acetoin:2,6-dichlorophenolindophenol oxidase acetoate dehydrogenase enzyme system.
A;Reference number: A39138; MUID:911003666
A;Accession: B39138
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <OOPP>

Query Match Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 EHSH 17
| | | |
Db 2 EHSH 5

C;Superfamily: dihydrolipoamide acetyltransferase; lipooyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A

Query Match Score 26; DB 2; Length 22;
Best Local Similarity 29.4%; Pred. No. 1e+03;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 RLIAFTSEHSHFSLKKG 23
| : | | : | : : |
Db 4 RILALTMPKKGLTMEEG 20

RESULT 6
IT3619 endothelial growth factor receptors fit [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: IT3619
R;Brocock, C.A.; Charnock-Jones, D.S.; Sharkey, A.M.; McLaren, J.; Barker, P.J.; WR
J. Natl. Cancer Inst. 87, 506-516, 1995
A;Title: Expression of vascular endothelial growth factor and its receptors fit and
A;Reference number: 156493; MUID:9522657
A;Accession: IT3619
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-24 <RES>
A;Cross-references: GB: S77814; NID: g998566; PIDN: AAB34002.1; PID: g998567
C;Genetics:
A;Gene: fit

Query Match Score 26; DB 2; Length 24;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 AFTEHSHF 18
| : | : |
Db 14 SFSSNYFH 22

RESULT 7
XGHENU urine glycopeptide - human
C;Species: Homo sapiens (man)
C;Accession: A03188
R;Loe, C.J.; Weiss, J.B.
Biochem. J. 123, 25P, 1971
A;Title: Identification in urine of a low-molecular-weight polar glycopeptide conta
A;Reference number: A03188; MUID:72062338
A;Accession: A03188
A;Molecule type: protein
A;Residues: 1-8 <LOT>
C;Comment: The identity of the glycoprotein from which this peptide is derived is u
re has also been found (see PIR:XHUE).
C;Keywords: glycoprotein
F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 EHSH 17
| | | |
Db 2 EHSH 5

RESULT 8
A28563 hemoglobin chain III - earthworm (Lumbricus terrestris) (fragment)

C;Species: Lumbicus terrestris (common earthworm)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 04-Mar-2000
C;Accession: A28563
A;Title: Two globin chains in the giant annelid extracellular haemoglobins.
A;Reference number: A90337; MUID:87241210
A;Accession: A28563
A;Molecule type: protein
A;Residues: 1-22 <GOT>
C;Superfamily: globin; globin homology
C;Keywords: oxygen carrier

RESULT 9

S07232 Query Match 20.0%; Score 25; DB 2; Length 22;
ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - garden pea (frag
N;Alternative names: rubisco subunit-binding protein alpha chain
C;Species: Pisum sativum (garden pea)
C;Accession: S07232
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C;Accession: S07232
R;Musgrave, J.E.; Johnson, R.A.; Ellis, R.J.
Eur. J. Biochem. 163, 529-534, 1987
A;Title: Dissociation of the ribulosebisphosphate-carboxylase large-subunit binding prot
A;Reference number: S07232; MUID:87161853
A;Accession: S07232
A;Molecule type: protein
A;Residues: 1-20 <WWS>
C;Comment: This protein binds the newly synthesized large subunit and the newly imported
C;Superfamily: chaperonin groEL
C;Keywords: chloroplast; heterododecamer; molecular chaperone

Query Match 19.6%; Score 24.5; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 9 IAFTSERSHPSLRKG 23
Db 5 IAF-DQHSSSAMQG 18

RESULT 10

A53875 Query Match 19.2%; Score 24; DB 2; Length 22;
creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C;Accession: A53875
R;White, K.C.; Babbitt, P.C.; Buchter, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 439-494, 1992
A;Title: The principal islet of the coho salmon (Oncorhynchus kisutch) contains the BB 1s
A;Reference number: A53875; MUID:93080727
A;Accession: A53875
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-20 <WHL>
A;Experimental source: Brockmann body, Principal islet
A;Note: sequence extracted from NCBI backbone (NCBIP-120599)
C;Superfamily: creatine kinase; creatine kinase repeat homology
C;Keywords: phosphotransferase

RESULT 11

S40638 Query Match 19.2%; Score 24; DB 2; Length 22;
ATP-43 protein - human (fragments)
C;Species: Homo sapiens (man)
C;Accession: S40638
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
R;Hurst, H.C.; Ratty, N.F.; Jones, N.C.
Nucleic Acids Res. 19, 4601-4609, 1991
A;Title: Identification and functional characterisation of the cellular activating t
A;Reference number: S40638; MUID:91367654
A;Accession: S40638
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <HUR>

RESULT 12

F84018 Query Match 19.2%; Score 24; DB 2; Length 22;
hypothetical protein BH2950 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: F84018
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliiphilic bacterium Bacillus halodurans
A;Accession: F84018
A;Status: preliminary
A;Molecule type: DNA
A;Reference number: A83650; MUID:20263314
A;Accession: F84018
A;Residues: 1-22 <STO>
A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06669.1; GSPDB
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2950

RESULT 13

J03611 Query Match 19.2%; Score 24; DB 2; Length 22;
vasoactive intestinal peptide - Atlantic cod (fragment)
C;Species: Gadus morhua (Atlantic cod)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Nov-1997
C;Accession: J03611
R;Thwaites, D.M.; Young, J.; Thorndyke, M.C.; Dimaline, R.
Regul. Pept. 21, 43-48, 1988
A;Title: Isolation and characterisation of two teleost VIP's.

A; Molecule type: protein
 A; Residues: 1-25 <RAW>
 C; Superfamily: glucagon
 C; Keywords: duplication; intestine; neuropeptide

Query Match Score 24; DB 2; Length 25;
 Best Local Similarity 35.7%; Pred. No. 2.4e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 11 FTSEHSHFSKKGA 24
 DB 6 FTDNYSRFRQMAA 19

RESULT 14

A60770 cell surface alloantigen gp60 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: A60770 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-Feb-1997
 R; Schadendorf, D.; Yamaguchi, H.; Old, L.J.; Srivastava, P.K.
 J; Immunol. 142, 1621-1625, 1989
 A;Title: A novel heteromorphic human cell surface alloantigen, gp60, defined by a human
 A;Reference number: A60770; MUID:89140352
 A;Accession: A60770
 A;Molecule type: protein
 A;Residues: 1-14 <SCH>
 C;Comment: This protein is an alloantigen in human populations but is not found on cells
 C;Comment: This protein exists in both membrane bound and cytosolic forms.
 C;Keywords: glycoprotein; polymorphism; surface antigen

Query Match Score 23; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 TAFTSHSHF 18
 DB 5 VSFTXESXGF 14

RESULT 15

PS0455 superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nipponbare) (fragment)
 C;Species: Oryza sativa (rice)
 C;Accession: PS0455
 R;Tsugita, A.
 submitted to JIPID, April 1993
 A;Reference number: PS0206
 A;Accession: PS0455
 A;Molecule type: protein
 A;Residues: 1-15 <TSU>
 A;Experimental source: germ
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; oxidoreductase

Query Match Score 23; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GNAALPHL 8
 DB 2 GIVALPL 9

Query Match Score 23; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRLLAF 11
 DB 2 PRLLF 7

RESULT 16
 PR0094:
 succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) 27k iron-sulfur protein, mitochondrial
 C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998
 C;Accession: PR0094
 R; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
 submitted to JIPID, July 1998
 A;Description: Proteome analysis of mouse brain.
 A;Reference number: PR0091
 A;Accession: PR0094
 A;Molecule type: protein
 A;Residues: 1-15 <KAW>
 A;Experimental source: brain, striatum
 C;Keywords: mitochondrion; oxidoreductase

Query Match Score 23; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAAPRLIAF 11
 DB 6 AAAPRKKF 14

RESULT 17

S66627 tau protein - human (fragments)
 C;Species: Homo sapiens (man)
 C;Accession: S66627
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 R; Moreno, F.J.; Medina, M.; Perez, M.; Montejo de Garcini, E.; Avila, J.
 FEBS Lett. 372, 65-68, 1995
 A;Title: Glycogen synthase kinase 3 phosphorylates recombinant human tau protein at
 A;Reference number: S66627; MUID:9602547
 A;Accession: S66627
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8;3-18 <MOR>

Query Match Score 23; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 SHPSLKKG 23
 DB 3 STENLKKG 10

RESULT 18

A17267 complement C4 - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Accession: A17267
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 30-Sep-1993
 R; Goldberger, G.; Abraham, G.N.; Williams, J.; Colten, H.R.
 J. Biol. Chem. 255, 7071-7074, 1980
 A;Title: NH2-terminal sequence analysis of Pro-C4, the precursor of the fourth comp
 A;Reference number: A17267; MUID:80227885
 A;Accession: A17267
 A;Molecule type: protein
 A;Residues: 1-22 <GOL>
 A;Note: 18-Val was also found
 C;Superfamily: alpha-2-macroglobulin

Query Match Score 23; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRLLAF 11
 DB 2 PRLLF 7

RESULT 19 R8633
 protein T17H7.9 [imported] - Arabidopsis thaliana (mouse ear cress)
 C;Species: Arabidopsis thaliana (mouse ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: R86433
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huijar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:2106719
 A;Accession: H06433
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-22 <STO>
 A;Cross-references: GB:AE005172; NID:94926824; PIDN:AAD32934.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: TI7H7.9
 A;Map position: 1
 RESULT 20 PH0858
 Maud protein - Paracoccus denitrificans (fragment)
 C;Species: Parrococcus denitrificans
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C;Accession: PH0858
 R;Chistoserdov, A.Y.; Boyd, J.; Mathews, F.S.; Lidstrom, M.E.
 Biochem. Biophys. Res. Commun. 184, 1181-1189, 1992
 A;Title: The genetic organization of the mau gene cluster of the facultative autotroph P. denitrificans
 A;Reference number: PH0856; MUID:92272706
 A;Accession: PH0858
 A;Molecule type: DNA
 A;Residues: 1-23 <CHT>
 A;Cross-references: GB:M90098; NID:9150580; PIDN:AAA25577.1; PID:9150581
 C;Genetics:
 C;Genetics: maud
 Query Match 18.4%; Score 23; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred. No. 3.1e+03; Indels 5; Conservative 1; Mismatches 2; Gaps 0; Matches 5; Indels 0; Gaps 0;
 QY 13 SEHSFSL 20.
 || : |||
 Db 13 SERNFFSL 20
 RESULT 21 A36912
 hypothetical protein 1 baiG-region [imported] - Eubacterium sp. (fragment)
 C;Species: Eubacterium sp.
 C;Accession: A36912
 R;Franklund, C.V.; Baron, S.F.; Hylemon, P.B.
 J. Bacteriol. 175, 3002-3012, 1993
 A;Title: Characterization of the baiG gene encoding a bile acid-inducible NADH:flavin ox
 A;Reference number: A36912; MUID:9325945
 RESULT 22 S09363
 hypothetical MTCO1/MTCYB mutant fusion protein - human mitochondrion (fragment)
 C;Species: mitochondrial Homo sapiens (man)
 C;Date: 21-Nov-1993 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000
 C;Accession: S09363
 R;Poulton, J.; Deadman, M.E.; Gardiner, R.M.
 Nucleic Acids Res. 17, 10223-10229, 1989
 A;Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy:
 A;Reference number: S09363; MUID:90098864
 A;Accession: S09363
 A;Gene: MTCO1/MTCYB
 A;Genome: mitochondrion
 A;Genetic code: SGCI
 C;Keywords: fusion protein; mitochondrion
 F114/Region: cytochrome-c oxidase chain I
 F114/Region: cytochrome b (+2 frame shifted)
 RESULT 23 S74176
 Query Match 18.4%; Score 23; DB 4; Length 24;
 Best Local Similarity 66.7%; Pred. No. 3.4e+03; Indels 4; Conservative 1; Mismatches 1; Gaps 0; Matches 4; Indels 0; Gaps 0;
 QY 17 HPSLKK 22
 ||||:
 Db 7 HPSLTK 12
 RESULT 24 S74176
 glutokinase (EC 2.7.1.12); thermoresistant - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
 C;Accession: S74176
 R;Izuhara, H.; Adachi, O.; Yamada, M.
 FEBS Lett. 394, 14-16, 1996
 A;Title: Purification and characterization of the Escherichia coli thermoresistant g
 A;Reference number: S74176; MUID:97074194
 A;Accession: S74176
 A;Molecule type: protein
 A;Residues: 1-10 <IZU>
 A;Experimental source: strain K-12
 A;Gene: gntK
 C;Keywords: dimer; phosphotransferase
 C;Genetics:
 C;Genetics: gntK
 Query Match 17.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+03; Indels 3; Conservative 1; Mismatches 2; Gaps 0;
 Matches 3; Indels 0; Gaps 0;
 QY 12 TSESH 17

```
1: 1 |
Db 2 TTNHDH 7
```

RESULT 24

S01122
 photosystem II 3.7K protein - spinach (fragment)
 C;Species: Spinaciaoleracea (spinach)
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: S01122
 R;Schroeder, W.P.; Hentysson, T.; Akerlund, H.E.
 FEBS Lett. 235, 289-292, 1988
 A;Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
 A;Reference number: S01120
 A;Accession: S01122
 A;Molecule type: protein
 A;Residues: 1-12 <SCH>
 C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
QY	5 LPRLIAFS 13	17.6%	22	DB 2;	Length 12;			
Db	2 LPEAYAFLS 10	55.6%	2	Pred.	No. 2.4e+03;	0	0	0;

RESULT 25

PH1635
 Ig H chain V-D-J region (clone B-less 218) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1635
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609
 A;Accession: PH1635
 A;Molecule type: DNA
 A;Residues: 1-12 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
QY	3 AALPRLIAF 11	17.6%	22	DB 2;	Length 12;			
Db	2 AGLPGLIICY 10	44.4%	2	Pred.	No. 2.4e+03;	3	0	0;

Search completed: January 6, 2002, 09:53:18
 Job time: 229 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: January 6, 2002, 09:52:34 ; Search time 12.98 Seconds
(without alignments)
70.618 Million cell updates/sec

Title: Perfect score:
Sequence: US-09-441-061-2
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Maximum Match 0%
Listing first 50 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

§

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	28.5	22.8	21	1	MISG_MISAN	P81474 misgurnus a
2	26	20.8	25	1	CRI1_LITSP	P56226 litoria spl
3	26	20.8	25	1	CRI2_LITSP	P56227 litoria cae
4	26	20.8	25	1	CRI3_LITSP	P56228 litoria cae
5	26	20.8	25	1	CRI4_LITSP	P56229 litoria gil
6	25	20.0	8	1	GLUR_HUMAN	P02779 homo sapien
7	25	20.0	24	1	FRE4_LITSP	P82023 litoria inf
8	24	19.2	25	1	CRI5_LITSP	P56230 litoria cae
9	10	19.2	25	1	VIP_GADMO	P09684 gadus morhu
10	23	18.4	12	1	PV12_PERAM	P81555 periplaneta
11	23	18.4	22	1	CO4_CAVPO	P19069 cavia porce
12	22.5	18.0	23	1	CH00_THIIE	P29134 thiobacillus
13	22	17.6	13	1	LMT4_LOM1	P41940 locusta mig
14	22	17.6	18	1	CYCH_MOUSE	P01458 mus musculus
15	21	16.8	18	1	PART_ASCSU	P43171 ascaris suu
16	21	16.8	16	1	LPHL_ECOLI	P03058 escherichia
17	21	16.8	22	1	SETB_SALTY	P33027 salmonella
18	21	16.8	24	1	GABE_RANRU	P80400 rana rugosa
19	20	16.0	8	1	ALLI_CYDPO	P82152 cydia pomon
20	20	16.0	10	1	GLEM_HUMAN	P02728 homo sapien
21	20	16.0	10	1	GONI_PETMA	P04378 petromyzon
22	20	16.0	15	1	ASPL_LACSN	P82648 lactobacillus
23	20	16.0	15	1	MCA2_RHOOP	P56870 rhodococcus
24	20	16.0	20	1	DFIS_RAT	P07448 rattus norve
25	20	16.0	20	1	LPTR_BACST	P05658 bacillus st
26	20	16.0	22	1	CYSP_TRIVIA	P33404 trichomonas
27	20	16.0	24	1	LPER_STRIER	P45440 streptomyces
28	20	16.0	25	1	SCRK_LACTIA	P09124 lactococcus
29	19.5	15.6	25	1	G3P2_JACOR	P80447 jaculus ori
30	19	15.2	10	1	GNOL_ALLMI	P37041 alligator m
31	19	15.2	16	1	CXAL_CONNL	P56639 conus aulic
32	19	15.2	18	1	AL3_CARMA	P81816 carinus ma
33	19	15.2	1	ATPB_CANFA	P99504 canis famili	

ALIGNMENTS

RESULT 1
MISG_MISAN STANDARD; PRT; 21 AA.
ID MISG_MISAN
AC P81474;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MISGRIN.
OS Misgurnus anguillicaudatus.
OC Bækayota; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ostariophysi; Actinopterygii; Neopterigii; Teleostei; Euteleoste; Ostariophysi; Cypriniformes; Cobitidae; Misgurnus.
OC NCBI-TaxID=75329;
RN [1]
RP SEQUENCE.
RX MEDLINE-9715401; PubMed-97271200;
RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
RT "A novel antimicrobial peptide from the loach, Misgurnus anguillicaudatus";
RT FEBS Lett. 411:173-178(1997).
CC - FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.
CC - MASS SPECTROMETRY: MW=2502; METHOD=MALDI.
KW Antimicrob; fungicide.
SQ SEQUENCE 21 AA; 2502 MW; 4A6ED0DAB391BCF1 CRC64;

Query Match Best Local Similarity 22.8%; Score 28.5; DB 1; Length 21; Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QV 14 EHSHPSLKKGA 25
Db 6 BLSKFS-KKGAA 16

RESULT 2
CR11_LITSP STANDARD; PRT; 25 AA.
ID CR11_LITSP
AC P56226;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 1.1.
OS Litoria splendida, Litoria gilleni, and Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
Litoria.
OC NCBI-TaxID=30345, 39405, 30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1 AND 1.1.2.

RC SPECIES="L. splendida"; TISSUE="Parotoid gland";
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caerins and
 caeridin 1 from Litoria splendida.";
 RL J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.2 AND 1.1.4.
 RC SPECIES="L.caerulea; TISSUE=Parotoid gland";
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea."
 RL J. Chem. Res. 138:930-936(1993).
 RN [3]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.3; 1.1.5 TO 1.1.8.
 RC SPECIES="L.gilleni"; TISSUE=Parotoid gland; Litoria splendida";
 RA Wong H.; Bowie J.H.; Carver J.A.;
 RT "The solution structure and activity of caerin 1.1, an antimicrobial
 peptide from the Australian green tree frog, *Litoria splendida*,";
 RL Eur. J. Biochem. 247:545-557(1997).
 CC -1- FUNCTION: ANTIBACTERIAL AND ANTIVIRAL PEPTIDES THAT ADOPT AN ALPHA
 HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 RP FUNCTION, AND STRUCTURE BY NMR.
 RC SPECIES="L.splendida";
 RX MEDLINE=97409981; PubMed=92666696;
 RA Stone D.J.M.; Waugh R.J.; Carver J.A.;
 RT "The solution structure and activity of caerin 1.1, an antimicrobial
 peptide from the Australian green tree frog, *Litoria splendida*,";
 RL Eur. J. Biochem. 247:545-557(1997).
 CC -1- FUNCTION: ANTIBACTERIAL AND ANTIVIRAL PEPTIDES THAT ADOPT AN ALPHA
 HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH
 CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY.
 CC -1- PTM: THE MAJOR PRODUCT IS CAERIN 1.1. IN ADDITION, DIFFERENT
 PEPTIDES ARE PRODUCED THAT ARE MISSING SOME AMINO ACID RESIDUES AT
 THE N-TERMINUS OR C-TERMINUS. ALL ISOFORMS ARE NOT REPRESENTED IN
 EACH SPECIES. CAERIN 1.1.1 AND CAERIN 1.1.4 ARE INACTIVE.
 CC -1- MASS SPECTROMETRY: MW=258.2; METHOD=FAB; RANGE=1-15.
 CC -1- MASS SPECTROMETRY: MW=241.2; METHOD=FAB; RANGE=3-35.
 CC -1- MASS SPECTROMETRY: MW=229.9; METHOD=FAB; RANGE=4-25.
 CC -1- MASS SPECTROMETRY: MW=142.1; METHOD=FAB; RANGE=1-25.
 CC -1- MASS SPECTROMETRY: MW=142.1; METHOD=FAB; RANGE=1-25.
 CC -1- MASS SPECTROMETRY: MW=233.7; METHOD=FAB; RANGE=1-16.
 CC -1- MASS SPECTROMETRY: MW=162.6; METHOD=FAB; RANGE=1-16.
 CC -1- MASS SPECTROMETRY: MW=148.9; METHOD=FAB; RANGE=1-15.
 CC -1- MASS SPECTROMETRY: MW=118.0; METHOD=FAB; RANGE=1-12.
 CC -1- MASS SPECTROMETRY: MW=91.5; METHOD=FAB; RANGE=1-10.
 KW Antibiotic; Antiviral; Amphibian skin; Amidation.
 FT PEPTIDE 1 25 CAERIN 1.1.
 FT PEPTIDE 3 25 CAERIN 1.1.1.
 FT PEPTIDE 4 25 CAERIN 1.1.2.
 FT PEPTIDE 13 25 CAERIN 1.1.3.
 FT PEPTIDE 1 23 CAERIN 1.1.4.
 FT PEPTIDE 1 16 CAERIN 1.1.5.
 FT PEPTIDE 1 15 CAERIN 1.1.6.
 FT PEPTIDE 1 12 CAERIN 1.1.7.
 FT PEPTIDE 1 10 CAERIN 1.1.8.
 FT MOD_RES 25 2558 MW; D8A5A460B0BE00 CRC64;
 SQ SEQUENCE 25 AA; 2585 MW;

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | : : : |
 Db 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

AC P56227; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIN 1.2.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Litoria.
 NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea.";
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY.
 CC -1- MASS SPECTROMETRY: MW=255.2; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 2555 MW; D8A5A460BB1464C0 CRC64;
 SQ SEQUENCE 25 AA; 2555 MW;

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | : : : |
 Db 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

CC CR13_LITCE STANDARD; PRT; 25 AA.
 ID CR13_LITCE STANDARD; PRT; 25 AA.
 AC P56228;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIN 1.3.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Litoria.
 NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea.";
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY.
 CC -1- MASS SPECTROMETRY: MW=258.2; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 2555 MW; D8A5A460BB0EA2F2 CRC64;
 SQ SEQUENCE 25 AA; 2555 MW;

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | : : : |
 Db 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

QY	5	LPRRIIAFSEH	15	Score 20.8%; Best Local Similarity 36.4%; Matches 4; Conservative	Score 26; DB 1; Length 25; Pred. No. 5.9e+02; Mismatches 3; Indels 4; Gaps 0;	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	14	LPHVVPVIAEH	24	CRC_4_LITGI	STANDARD; PRT; 25 AA.	NCBI_TaxID=9605; [1]	NCBI_TaxID=9605; [1]
RESULT	5			CR4_LITGI	STANDARD; PRT; 25 AA.	RN	SEQUENCE.
ID				AC	P56229; DR	RP	MEDLINE72062338; PubMed=5126885;
AC				DT	15-JUL-1998 (Rel. 36, Created)	RA	Lote C.J., Weiss J.B.;
DT				DT	15-JUL-1998 (Rel. 36, Last sequence update)	RT	"Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose.";
DT				DT	15-JUL-1998 (Rel. 36, Last annotation update)	RL	Biochem. J. 123:25P-25P(1971).
DE				DE	CAERIN 1.4.	CC	-1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A
OS				OS	Litoria gilleni, and Litoria caerulea.	CC	SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
OC				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;	DR	PIR; A03188; XSGHEU.
OC				OC	Litoria.	DR	Glycoprotein.
OX				OX	NCBI_TaxID=39405, 30344;	FT	CARBONID. 1 1 S-LINED (GAL. . .)
RN				RN	SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4.	SQ	SEQUENCE 8 AA; 855 MW; C2D8AA1F5B1EB1E CRC64;
RP				RP	SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4.1.		
RC				RC	SPCIES=L. gilleni; TISSUE=Parotoid gland;		
RA				RA	Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;		
RT				RT	"Peptides from Australian frogs. The structures of the caerins and caeridins from Litoria gilleni.";		
RL				RL	J. Chem. Res. 139:937-951(1993).		
CC				CC	-1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.		
CC				CC	-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.		
CC				CC	-1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY SIMILARITY).		
CC				CC	-1- MASS SPECTROMETRY: MW=6500; METHOD=FAB; RANGE=1-25.		
CC				CC	-1- MASS SPECTROMETRY: MW=933; METHOD=FAB; RANGE=1-10.		
KW				KW	Antibiotic; Amphibian skin; Amidation; FT		
FT				FT	PEPTIDE 1 25 CAERIN 1.4.		
FT				FT	PEPTIDE 1 10 CAERIN 1.4.1.		
MOD RES				MOD RES	25 25 AMIDATION.		
SQ				SQ	SEQUENCE 25 AA; 2603 MW; D8A5BEBA7DB80E000 CRC64;		
Query Match				Query Match	20.8%; Score 26; DB 1; Length 25; Best Local Similarity 36.4%; Pred. No. 5.9e+02; Mismatches 3; Indels 4; Gaps 0;		
Matches				Matches	20.0%; Score 25; DB 1; Length 24; Best Local Similarity 83.3%; Pred. No. 8.1e+02; Mismatches 5; Conservative		
QY	5	LPRRIIAFSEH	15	QY	20 LKKGAA 25	OC	Antibiotic; Amphibian skin.
Db	14	LPHVVPVIAEH	24	Db	6 LKKGAS 11	CC	SEQUENCE 24 AA; 2495 MW; 6986D063947805A1 CRC64;
RESULT	6			RESULT	8	CC	SEQUENCE.
ID		GLUR_HUMAN	STANDARD:	ID	CR5_LITCE	CC	CR5_LITCE
ID		GLUR_HUMAN	STANDARD:	ID	CR5_LITCE	CC	CR5_LITCE
AC		P02729; 21-JUL-1986 (Rel. 01, Created)	PRT: 8 AA.	AC	P56230; 15-JUL-1998 (Rel. 36, Created)	AC	P56230; 15-JUL-1998 (Rel. 36, Last sequence update)
DT		21-JUL-1986 (Rel. 01, last sequence update)		DT	15-JUL-1998 (Rel. 36, Last sequence update)	DT	15-JUL-1998 (Rel. 36, Last annotation update)
DT		20-AUG-2001 (Rel. 40, Last annotation update)		DE	Homo sapiens (Human).	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Best Local Similarity 35.7%; Pred. No. 1.2e+03; Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

DE CAERIN 1.5.
 OS Litoria caerulea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Litoria;
 OX NCBI_TaxID=30344;
 RN [1]
 RP SOURCE, AND MASS SPECTROMETRY.
 RC TISSUE-Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.C., Wallace J.C., Tyler M.J.;
 RT Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea.;
 RT Litoria caerulea.;
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE-SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELIX AND GREATER FLEXIBILITY (BY
 SIMILARITY).
 CC -1- MASS SPECTROMETRY: MW=2610; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 25 AMIDATION.
 SQ SEQUENCE 25 AA: 2613 MW: OFF5A164EAQEBE12 CRC64;

Query Match Score 24; DB 1; Length 25;
 Best Local Similarity 19.2%; Pred. No. 1.2e+03; Matches 4; Indels 0; Gaps 0;

QY 5 IPRLIARTSEH 15
 :| :: :||:
 DB 14 IPHVVPVTAEH 24

RESULT 9
 VIP_GADMO STANDARD PRT; 25 AA.
 AC P09684;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE Vasoactive Intestinal Peptide (VIP) (FRAGMENT).
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae;
 OC Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RA Thwaites D.T., Young J., Thorndyke M.C., Dimaline R.;
 RT Isolation and characterisation of two teleost VIP's.;
 RL Regul. Pept. 21:436-436 (1988).
 CC -1- FUNCTION: VIP CAUSES VASODILATATION, LOWERS ARTERIAL BLOOD
 PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 AND GALL BLADDER.
 CC -1- MISCELLANEOUS: THERE IS ONLY A SINGLE DIFFERENCE BETWEEN THIS
 CC SEQUENCE AND THAT OF CHICKEN (ALA-19 INSTEAD OF VAL-19).
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; JQ0611; JQ0611.
 DR InterPro; IPR00032; Glucagon.
 DR Pfam; PF00123; hormone2_1.
 DR SMART; SM00070; GLUCA_1.
 DR PS00260; GLUCAGON_1.
 KW Glucagon family; Hormone.
 FT NON_TER 25 25 ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C1A
 SQ SEQUENCE 25 AA: 2978 MW: 1573FF6F374DB7E4 CRC64;

Query Match Score 24; DB 1; Length 25;

Best Local Similarity 35.7%; Pred. No. 1.2e+03; Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 11 FTSSHSHSFSLKGA 24
 DB 6 FTDNYSRFRQMAA 19

RESULT 10
 PVK2_PERAM STANDARD PRT; 12 AA.
 ID PVK2_PERAM
 AC P81555;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PERIVISCROKININ-2 (PEA-PVK-2).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattidae; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;

RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisynaptic organs;
 RX MEDLINE=98326577; Pubmed=9653444;
 RA Predeel R., Repus J., Eckert M., Holman G.M., Nachman R.J., Wang Y., Penzin H.,
 RA "Isolation of Periviscerokinin-2 from the abdominal perisynaptic organs of the American cockroach, *Periplaneta americana*.";
 RL Peptides 19:801-809(1998).
 CC -1- FUNCTION: MYOATONIC PEPTIDE; HAS EXCITATORY ACTIONS ON THE HYPERNEURAL MUSCLE.
 CC -1- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI.
 KW Neuropeptide; Amidation.
 FT MOD_RES 12 12 AMIDATION
 SQ SEQUENCE 12 AA: 1190 MW: 2F4D8EEE1EB05728 CRC64;

Query Match Score 23; DB 1; Length 12;
 Best Local Similarity 18.4%; Pred. No. 8.2e+02; Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMAPRL8
 :| :||:
 DB 5 GLISMPPRV 12

RESULT 11
 CO4_CAVPO STANDARD PRT; 22 AA.
 ID CO4_CAVPO
 AC P19699;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE COMPLEMENT C4 (FRAGMENT).
 GN C4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hstricognathi; Caviidae.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80227885; PubMed=7391069;
 RA Goldberger G., Abraham G.N., Williams J., Colten R.R.;
 RT "NH2-terminal sequence analysis of pro-C4, the precursor of the fourth component of guinea pig complement.";
 RT J. Biol. Chem. 255:7071-7074(1980).
 CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY ANAPHYLATOXIN.
 CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C1A
 CC AND, PRIOR TO SECRETION, IS ENZYMATIICALLY CLEAVED TO FORM A TRIMER

* OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).

CC

DR

PIR; A17267; A17267.

DR

InterPro; IPR01599; Alpha_2_macroglobin.

DR

InterPro; IPR000020; Anaphylatoxin.

DR

PROSITE; PS00477; ALPHA_2_MACROGLOBULIN_PARTIAL.

DR

PROSITE; PS01177; ANAPHYLATOXIN_1; PARTIAL.

KW

Complement pathway; Plasma; MHC III; Inflammatory response.

FT

VARIANT 18 L->V.

FT

NON_TER 22 22

SEQUENCE 22 AA; 2452 MW; 2CD16B54D0BB47A4 CRC64;

SQ

Query Match 18.4%; Score 23; DB 1; Length 22;

Best Local Similarity 66.7%; Pred. No. 1.5e+03; 1; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRLLAF 11.

Db 2 PRLLF 7

RESULT 12

CH60_THIE

STANDARD;

PRT;

23 AA.

AC

P29134;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).

GN GROEL OR MOPA OR GROEL

OS Thiobacillus ferrooxidans.

OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.

OX NCBI_TAXID=920;

RN [1]

RP SEQUENCE.

RC STRAIN=AVCC 19859;

RX MEDLINE=93093401; PubMed=1360930;

RA Varela P.; Jerez C.A.;

RT "Identification and characterization of GROEL and DnaK homologues in

RT Thiobacillus ferrooxidans";

RL FEMS Microbiol. Lett. 77:149-153(1992).

RN [2]

RP PHOSPHORYLATION.

RX MEDLINE=96242312; PubMed=9026439;

RA Seeger M.; Osorio G.; Jerez C.A.;

RT "Phosphorylation of GroEL, DnaK and other proteins from Thiobacillus ferrooxidans grown under different conditions";

RL FEMS Microbiol. Lett. 138:120-134(1996).

-I- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

CC -I- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STAKED RINGS OF

CC 7 SUBUNITS.

CC -I- INDUCTION: BY HEAT SHOCK.

CC -I- PTM: PHOSPHORYLATED ON THREONINE.

CC -I- MISCELLANEOUS: THIS PROTEIN SHOWS ATPASE ACTIVITY.

CC -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

DR HSSP; P06139; IAO1'.

DR InterPro; IPR01840; Chaperonins_Cpn60.

DR PROSITE; PS0096; CHAPERONINS_CPN60; PARTIAL.

KW Chaperone; ATP-binding; Heat shock; Phosphorylation.

FT NON_TER 23 23

SEQUENCE 23 AA; 2536 MW; 2BB6883872FB255D CRC64;

Query Match 18.0%; Score 22.5; DB 1; Length 23;

Best Local Similarity 33.3%; Pred. No. 1.9e+03; 1; Indels 1; Gaps 1;

Matches 5; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 9 IAPTFSEHSRHSLSKG 23

Db 5 VAF-REHAREKMLRG 18

RESULT 13

LMT4_LOCMI

STANDARD;

PRT;

13 AA.

ID LMT4_LOCMI

STANDARD;

PRT;

13 AA.

AC P1490;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE LOCUSTAMYTROPIN 4 (LOM-MT-4).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Acridoidea; Orthopteroidea; Orthoptera; Caelifera;

OC Acrideromorpha; Acridoidea; Acridae; Locusta.

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUEBrain; Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,

RA Schoofs L., de Loof A.;

RT de Loof A.;

RT "Isolation, identification and synthesis of locustamytropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamytropin peptide family";

RT Insect Biochim. Mol. Biol. 22:447-452(1992).

RL CC -I- FUNCTION: POTENT MODULATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE STIMULATOR THAN LOM-MT I, II AND III.

CC -I- SIMILARITY: BELONGS TO THE PYRORININ FAMILY.

DR InterPro; IPR01484; Pyrarinin.

DR PROSITE; PS00539; PYRORININ; I.

KW Neuropeptide; Amidation; Pyrarinin.

FT MOD_RES 13 13

SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 13;

Best Local Similarity 62.5%; Pred. No. 1.3e+03; 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GMALPRL 8

DB 6 GMFPSPRL 13

RESULT 14

CYCH_MOUSE

STANDARD;

PRT;

18 AA.

ID CYCH_MOUSE

STANDARD;

PRT;

18 AA.

AC Q61458;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CYCLIN H (FRAGMENT).

GN CENH.

OS MUS musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NEBL_TAXID=10090;

RN [1]

RP SEQUENCE FROM N A.

RC STRAIN=CD-1; TISSUE=Testis;

RA Hall F.L., Wu L.;

RL Submitted (Nov-1994) to the EMBL/GenBank/DBJ databases.

CC -I- FUNCTION: MEMBER OF CKAK WHICH ACTIVATES CYCLIN ASSOCIATED CDK2/CDK2/CDK4 BY THREONINE PHOSPHORYLATION. ITS EXPRESSION AND ACTIVITY ARE CONSTANT THROUGHOUT THE CELL CYCLE. CKAK IS TIGHTLY ASSOCIATED WITH A MULTIPROTEIN COMPLEX CKAK, WHICH PLAYS A DUAL ROLE IN TRANSCRIPTION AND DNA REPAIR (BY SIMILARITY).

CC -I- SUBUNIT: MAMMALIAN CKAK CONTAINS THREE COMPONENTS: CDK7, CYCLIN H,

CC -I- AND AN ASSEMBLY FACTOR CALLED MAT1.

CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.

CC

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC DR EMBL: X82441; CAA57822; 1; -
 CC DR HSP; P51946; 1KXU.
 CC DR Interro; IPR000553; Cyclin.
 CC DR PROSTE; PS00292; CYCLINS; PARTIAL.
 CC KW Cyclin; Cell cycle; Cell division; Nuclear protein;
 CC KW transcription regulation.
 FT NON_TER 1 1
 FT 18 AA; 2105 MW; 92964DCF68EB98C7 CRC64;
 SQ SEQUENCE 18 AA; 2105 MW; 92964DCF68EB98C7 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03; 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRLIJAF 12
 Db 10 PRIMLT 16

RESULT 15
 FAR7_ASCSU STANDARD PRT; 8 AA.
 ID FAR7_ASCSU STANDARD PRT; 8 AA.
 AC P4_71;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DT FMRFamide-like neuropeptide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TAXID=6233;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=295380362; PubMed=7651904.
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
 RT Ascaris suum";
 RL Peptides 16:491-500(1995).
 CC -I SIMILARITY: BEIJING TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 963 MW; 9CD40059DA17687D CRC64;

Query Match 16.8%; Score 21; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRLIJAF 11
 Db 3 PREFRF 8

RESULT 16
 LPHI_ECOLI STANDARD PRT; 16 AA.
 ID LPHI_ECOLI STANDARD PRT; 16 AA.
 AC P03058;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HIS OPERON LEADER PEPTIDE (ATTENUATOR PEPTIDE).
 GN HISL OR B2018.
 OS Escherichia coli, and Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia, NCBI_TAXID=562, 602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; and S.typhimurium; STRAIN=K12, AND LT2;
 RX MEDLINE=89034829; PubMed=306217;
 RA Carlonagno M.S., Chiariotti L., Alifano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the *Salmonella typhimurium* and *Escherichia*
 coli K-12 histidine operons." J. Mol. Biol. 203:585-606(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=82039525; PubMed=617094;
 RA Verde P., Frunzio R., di Nocera P.P., Blasi F., Bruni C.B.;
 RT "Identification, nucleotide sequence and expression of the regulatory
 region of the histidine operon of *Escherichia coli* K-12." Nucleic Acids Res. 9:2075-2086(1981).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=79033821; PubMed=360215;
 RA Dincera P.P., Blasi F., Dilauro R., Frunzio R., Bruni C.B.;
 RT "Nucleotide sequence of the attenuator region of the histidine operon
 of *Escherichia coli* K-12." Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97122661; PubMed=3278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12." Science 277:1453-1474 (1997).
 RL [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2;
 RX MEDLINE=79033822; PubMed=360216;
 RA Barnes W.M.;
 RT DNA sequence from the histidine operon control region: seven
 histidine codons in a row";
 RL Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE ATTENUATION MECHANISM
 CC FOR THE CONTROL OF THE EXPRESSION OF THE HIS STRUCTURAL GENES.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC DR EMBL; V00385; CAA23350; 1; -
 CC DR EMBL; V00384; CAA23348; 1; -
 CC DR EMBL; X13662; CAA3101; -
 CC DR EMBL; V0131; CAA24556; 1; -
 CC DR EMBL; AE000293; AAC15079; 1; -
 CC DR EMBL; X1366; CAA3121; 1; -
 CC DR EMBL; J01804; AAA8813; 1; -
 CC DR PIR; A03594; LFPECH
 DR Ecogene; BG1129; hisL.
 DR StyGene; SG10166; hisL.
 KW Histidine biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 16.8%; Score 21; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 2.3e+03; Mismatches 5; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 IAFTSHSH 17
 Db 4 VQFKHHHH 12

RESULT 17
 SETB_SALTY STANDARD PRT; 22 AA.

ID SETB_SALTY STANDARD; PRT; 22 AA.

AC P33027;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SUGAR_EFLUX TRANSPORTER_B (FRAGMENT)

GN SETB.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TAXID=602;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=8931364; PubMed=2546043;
 RA Geerse R.H., Izzo P.W.; Postma P.W.;
 RT "The PEP: fructose 6-phosphate transferase system in *Salmonella* L-Mol. Gen. Genet. 216:517-525(1989).
 RL MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN
 CC TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 (PROBABLE);
 CC -!- SIMILARITY: BELONGS TO THE SET FAMILY OF TRANSPORTERS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; X14243; -; NOT_ANNOTATED_CDS.

DR STyGene; SG10423; setB.
 DR Transport; Sugar transport; Transmembrane; Inner membrane.
 FT TRANSPER 13 >22 POTENTIAL.
 FT NON_TER 22 22
 SEQUENCE 22 AA; 2291 MW; 2849C330172CC5C2 CRC64;

Query Match 16.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 45.5%; Pred. No. 3.2e+03; Mismatches 5; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 ALAPRILAFFS 13
 Db 7 AAAFRSFDTI 17

RESULT 18
 GAE6_RANRU STANDARD PRT; 24 AA.

ID GAE6_RANRU; STANDARD; PRT; 24 AA.

AC P80400;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE GREGORINI6.
 OS *Rana rugosa* (Frog); Eukaryota; Metazoa; Chordata; Craniata; vertebrates; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

Query Match 16.0%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05; Mismatches 3; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 SEHSHFSL 20
 Db .1 SPHNFGL 8

RESULT 20
 GLEM_HUMAN STANDARD PRT; 10 AA.

ID GLEM_HUMAN; STANDARD; PRT; 10 AA.

AC P02728;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

OX NCBI_TAXID=8410;
 RN [1] SEQUENCE.
 RP TISSUE=Skin;
 RX MEDLINE=55091844; PubMed=7999137;
 RA Park J.M., Jung J.-B., Lee B.J.;
 RT "Antimicrobial peptides from the skin of a Korean frog, *Rana rugosa*.";
 RL Blochem. Biophys. Res. Commun. 205:948-954(1994).
 RT "Amphibian skin: Antibiotic activity against both gram positive and gram negative bacteria, fungi and protozoa.";
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: SKIN.
 CC -!- SIMILARITY: BELONGS TO THE BREVINTIN/ESCUENTIN/GAEGURIN/RUGOSIN FAMILY.
 CC KW Amphibian skin; Antibiotic.
 FT DISCFFID 18 24
 SQ SEQUENCE 24 AA; 2610 MW; 09918123FF90CCFD CRC64;

Query Match 16.8%; Score 21; DB 1; Length 24;
 Best Local Similarity 54.5%; Pred. No. 3.5e+03; Mismatches 1; Indels 2; Gaps 1;
 Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 GMAA-LPRLL 9
 Db 7 GLAANFLPFTI 17

RESULT 19
 ALLI_CYDPO STANDARD PRT; 8 AA.

ID ALLI_CYDPO STANDARD; PRT; 8 AA.

AC P82152;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CYDSTATIN 1.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tortricoidea; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TAXID=82600;
 RN [1]
 RP SEQUENCE.

RC TISSUE=larva;

RX MEDLINE=98054539; PubMed=932829;
 RA Dube H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East D.D., Thorpe A.;
 RT "Lepidopteran Peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 MOD RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 934 MW; C82879C4551F775 CRC64;

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ERTHROCYTE MEMBRANE GLYCOPAPTIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE="2034940; PubMed=5286856;"
RA Weiss J.B., Lotz C.J., Bobinski H.;
RT "New low molecular weight glycopptide containing triglycosylcysteine
in human erythrocyte membrane."
RL Nature New Biol. 234:25-26(1971).
CC -1 PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
CC -1 MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED.
CC PIR: A03187; XGHDB.
KW Glycoprotein; Erythrocyte.
FT CABHOHD 1 Erythrocyte.
SEQUENCE 10 AA; 1049 MW; 239BFEEAA1F5B1E8 CRC64;
SQ S-LINKED (GLC-
1 1
1 1)
1 1
1 1 .
Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mishatches 0;
Indels 0; Gaps 0;
Qy 15 HSH 17
Db 4 HSH 6
Result 21
GONI_PETMA STANDARD; PRT; 10 AA.
ID GONI_PETMA
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GONADOLIBERIN I (GONADOTROPIN RELEASING HORMONE I) (GNRH-I)
DE (LUTLIBERIN I)
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
RN [1] NCBI_TaxID=7757;
RP SEQUENCE.
RC TISSUE_Brain;
RX MEDLINE="86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT Primary structure of gonadotropin-releasing hormone from lamprey
brain.';
RL J. Biol. Chem. 261:4812-4819(1986).
CC -1 FUNCTION: STIMULATES THE TERMINATION OF BOTH LUTEINIZING AND
FOLLICLE-STIMULATING HORMONES.
CC -1 SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR: A01412; RHMNGS.
DR InterPro: IPR002012; Gnrh.
DR Pfam: PF00446; Gnrh_1.
DR PROSITE: PS00473; GNRH_1.
KW Hormone; Amidation; Hypothalamus.
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 AMIDATION.
SEQUENCE 10 AA; 1244 MW; 1E4B16237B1735AB CRC64;
SQ [1]
Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mishatches 0;
Indels 0; Gaps 0;
Result 22
ASPL_LACSN STANDARD; PRT; 15 AA.
ID ASPL_LACSN
AC P82618;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ACID SHOCK PROTEIN 1 (FRAGMENTS).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Bacillales/Clostridiales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1;
RX Published=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbi M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -1 INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;
Qy 19 SLKKG 23
Db 1 SFRKKG 5
Result 23
MCA2_RHOOP STANDARD; PRT; 15 AA.
ID MCA2_RHOOP
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE PUTATIVE MALEYLACTATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriidae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
RN [1]
RP SEQUENCE.
RC STRAIN=LCP;
RX MEDLINE="98324954; PubMed=9057989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylactate reductase encoding region from
Rhodococcus opacus LCP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -1 CATALYTIC ACTIVITY: 3-OXOALIDATE + NAD(P)(+) = 2-MALEYLACETATE +
NAD(P)H.
CC PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -1 SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL-DEHYDROGENASE
FAMILY.
DR InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH-IRON_1; PARTIAL.
DR PROSITE: PS00060; ADH-IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NOR_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD0388025E CRC64;
Qy 17 HFSLK 21
Db 2 RYSLE 6
Query Match 16.0%; Score 20; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPRLTAF 11
| : |
ID DFTS_RAT STANDARD; PRT; 20 AA.
AC P0748;
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DB DENTINAL FLUID TRANSPORT-STIMULATING PEPTIDE (DFT-STIMULATING PEPTIDE).
DE PEPTIDE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Parotid gland;
RX MEDLINE=87131231; PubMed=3815601;
RA Yamamoto T., Kobayashi M., Kobayashi M., Yamamoto M., Nomura M.,
RA Aonuma S.;
RT "Isolation and amino acid sequence of dentinal fluid transport-
stimulating peptide from rat parotid glands.";
RL Chem. Pharm. Bull. 34:3803-3811(1986).
RN [2]
CHARACTERIZATION.
RX MEDLINE=67131708; PubMed=5297832;
RA Steinman R.R.;
RT "The movement of acriflavine hydrochloride through molars of rats on
a cariogenic and non-cariogenic diet.";
RT J. South. Calif. Dent. Assoc. 35:151-157(1967).
RL PIR; JJ001; DIR;
CC WHICH IS IMPORTANT FOR THE PREVENTION OF DENTAL CARIES.
DR Dental caries; Parotid gland; Hormone.
KW SEQUENCE 20 AA; 2165 MW; FA164F2B0AF80D5A CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
Best Local Similarity 27.8%; Pred. No. 4.2e+03; Mismatches 5; Conservative 4; Matches 9; Indels 0; Gaps 0;

QY 8 LIATTSERHSFSLKKGAA 25
Db 2 VIAVELQHNEPGRKDSTA 19

RESULT 25
LPTR_BACST STANDARD; PRT; 20 AA.
ID LPTR_BACST STANDARD; PRT; 20 AA.
AC P05258;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
GN TETL.
OS Bacillus stearothermophilus, Bacillus cereus, and
OS Staphylococcus hyicus.
OG Plasmid pTH15, Plasmid pBC16, and Plasmid pTETL.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Geobacillus.
OX NCBI_TaxID=1422; 1396, 1284;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=pTH15;
RX MEDLINE=86031344; PubMed=2996983;
RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
"Nucleotide sequence of the tetracycline resistance gene of pTH15, a

RT thermophilic *Bacillus* plasmid: comparison with staphylococcal *tcr* controls.;
RT Gene 37:131-138(1985).
RN [2]
SEQUENCE FROM N.A.
RC PLASMID=pBC15;
RX MEDLINE=90221899; PubMed=2109312;
RA Palva A., Virolainen G., Simonen M., Rintala H., Laamanen P.;
RT "Nucleotide sequence of the tetracycline resistance gene of pBC15 from *Bacillus cereus*.";
RL Nucleic Acids Res. 18:1635-1635(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S. hyicus; PLASMID=pTETL;
RX MEDLINE=92321725; PubMed=4622166;
RA Schwarz S., Cardoso M., Wedener H.C.;
"Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determinant encoded by plasmid pTETL from *Staphylococcus hyicus*".
RT Antimicrob. Agents Chemother. 36:580-588(1992).
RL CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC DR EMBL; D00006; BA00004.1; -.
DR EMBL; M11036; AA022850.1; -.
DR EMBL; X51366; CA035700.1; -.
DR EMBL; X60828; CA043219.1; -.
DR PIR; S09233; LFBSNU.
PIR; S23742; S23742.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CA1 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.2e+03; Mismatches 4; Conservative 4; Matches 4; Indels 0; Gaps 0;

QY 13 SEHSHFSLKKGAA 24
Db 4 NICCNRVOLKEGS 15

Search completed: January 6, 2002, 09:57:10
Job time: 276 sec

Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2002, 09:51:49; Search time 22.2 seconds

(without alignments)
164.721 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 125

Sequence: 1 GMALPRLIAFISSEHSHFSLKKGAA 25

Scoring table: BLOSUM62

Gapext 0.0, Gapext 0.5

Searched: 47505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SPREMBL-17:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phager:*

10: sp_plant:*

11: sp_ratodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	32	25.6	25 026056	O26056 helicobacte
2	30	24.0	6 P79337	P79337 prionialuru
3	27	21.6	25 040354	Q40354 medicago sa
4	26.5	21.2	24 097NS5	097NS5 homo sapien
5	26	20.8	9 Q9V82	09V82 drosophila
6	26	20.8	15 09TRP0	09TRP0 sus scrofa
7	26	20.8	23 Q9R314	Q9R314 helicobacte
8	26	20.8	4 Q16333	Q16333 homo sapien
9	25	20.0	15 09Z0U3	Q9Z0U3 rattus norv
10	25	20.0	5 Q9NbD9	Q9NbD9 chironomus
11	25	20.0	23 087081	Q87081 pseudorab
12	25	20.0	24 Q16061	Q16061 homo sapien
13	25	20.0	13 P82833	P82833 rana berlan
14	25	20.0	4 P82834	P82834 rana berlan
15	25	20.0	24 P82838	P82838 rana berlan
16	25	20.0	4 Q9BTR5	Q9BTR5 homo sapien
17	25	20.0	11 Q60839	Q60839 musculus
18	25	20.0	11 Q63999	Q63999 rattus norv
19	25	20.0	11 Q64000	Q64000 rattus norv

RESULT	1
ID	026056
AC	026056;
DT	01-JUN-1998 (TREMBLrel. 05', created)
DT	01-JUN-1998 (TREMBLrel. 14', last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14', last annotation update)
DE	HYPOTHETICAL 3.1 KDa PROTEIN.
GN	HP1528.
OS	Helicobacter pylori (Campylobacter pylori),
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC	Helicobacter.
OX	NCBI-TaxID=210;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=26695 / ATCC 700392;
RX	MEDLINE=97394467; PubMed=9352185;
RA	Tomb J.-F., White O., Kerecavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cottrell M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.B., Smith R.O., Fraser C.M., Venter J.C.;
RT	"The complete genome sequence of the gastric pathogen Helicobacter pylori";
RL	Nature 388:539-547(1997).
DR	EMBL: AB00511; AAC08577.1; TIGR: HP1528; KW: hypothetical protein; Complete proteome.
SEQUENCE	25 AA: 3075 MW: E080E93A41CQE396E CRC64;
SQ	Query Match 25.6%; Score 32; DB 2; length 25; Best Local Similarity 50.0%; Pred. No. 2.7e+02;

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., DT 01-JUN-2000 (TREMBrel. 14, Last annotation update),
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegnami C., DE DNA ADENINE METHYLASE HOMOLOG (FRAGMENT).
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., GN M_HFYI.
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., OS Helicobacter pylori (Campylobacter pylori).
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., MC Helicobacter; Helicobacter group;
 RA Merkulov G., Mishina N.V., Molarry C., Morris J., Mosirefi A., OX NBII_TAXID=210;
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., RN [1];
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacieb J.M., RP SEQUENCE FROM N_A.
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purli V., Reese M.G., RC STRAIN219, AND 213;
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Raudonikiene A., Berg D.E.;
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RT "iceA2 segment from H_pylori (Alaska strain 219)." ;
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X., RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., DR EMBL; AF00829; AAC4502; 1; -;
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., DR AF00828; AAC6500; 1; -;
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., KW Methytransferase.
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., FT NON-TER 23 23
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., SQ SEQUENCE 23 AA; 2635 MW; 6D6CCC65373742B3 CRC64;

Query Match 20.8%; Score 26; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 4.7e+05; PRT; 15 AA.
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 16 SHFSIKRGA 24 RESULT 8

Db 1 SHFSILNSA 9 ID Q16333 PRELIMINARY; PRT; 24 AA.

RESULT 6 ID Q9TRPO PRELIMINARY; PRT; 15 AA.

AC 09TRPO; AC Q16333; AC 016333;

DT 01-MAY-2000 (TREMBrel. 13, Created) DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)

DT 01-MAY-2000 (TREMBrel. 13, Last sequence update) DT 01-JUN-2000 (TREMBrel. 14, Last annotation update)

DE LOW MR ZONA PELLUCIDA BINDING PROTEIN (FRAGMENT).

OS Sus scrofa (Pig). DE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR (FRAGMENT).

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. RN FN RSEQUENCE FROM N_A.

RN RX MEDLINE=93378826; PubMed=1510840; OS Homo sapiens (Human); RX Boocock C.A., Charnock-Jones D.S., Sharkey A.M., McLaren J., RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; RA Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RT Barker P.J., Wright K.A., Twentyman P.R., Smith S.K.; NCBI_TAXID=9606;

[1] RT "Expression of vascular endothelial growth factor and its receptors fit and KDR in ovarian carcinoma";

RT J. Natl. Cancer Inst. 87:506-516(1995). DR EMBL; S77814; RAB34002; 1; -;

FT NON-TER 1 1

SQ SEQUENCE 24 AA; 2700 MW; 993CFEB9FE226A62 CRC64;

Query Match 20.8%; Score 26; DB 6; Length 15;
 Best Local Similarity 44.4%; Pred. No. 1.5e+03; PRT; 15 AA.
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAPRLIAF 11 RESULT 9

Db 1 |||...| 7 AAPPSWVF 15 ID Q9Z013 PRELIMINARY; PRT; 15 AA.

AC 09Z013; AC Q9Z013;

DT 01-MAY-1999 (TREMBrel. 10, Created) DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)

DT 01-MAY-2000 (TREMBrel. 13, Last sequence update) DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)

DE SNO ONCOPROTEIN (FRAGMENT).

GN SNO ONCOPROTEIN (FRAGMENT).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vedyo C.G., Sogayar M.C.;
 RT Cloning of glucocorticoid-regulated sequences using equalizing cDNA
 subtraction based on selective suppression of polymerase chain
 reaction in rat C6/ST1 glioma phenotypic reversion.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF112446; AAD17200.1;
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1667 MW; D2F5236DE2647B80 CRC64;

Query Match
 Best Local Similarity 20.0%; Score 25; DB 11; Length 15;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 16 SHFSIKGKA 24
 Db 6 SNFSIVQGS 14

RESULT 10

ID Q9NBD9 PRELIMINARY; PRT; 23 AA.

AC Q9NBD9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-NOV-2000 (TREMBLrel. 15, Last annotation update)

DE HEMOGLOBIN 1.1B (FRAGMENT).

GN GB2B.

OS Chironomus neapeanensis.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomoidea; Chironomidae; Chironominae; Chironomus.

OC Chironomoidea; Chironomidae; Chironominae; Chironomus.

OX NCBI_TAXID=13501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336639; PubMed=10876092;

RA Grushl M.C., Scherbk S.V., Almanova K.G., Blinov A., Diez J.-L.,
 RA Beigtron G.; Scherbk S.V., Almanova K.G., Blinov A., Diez J.-L.,
 RT "Insect globin gene polymorphisms: Intronic minisatellites and a
 RT retroposon interrupting exon 1 of homologous globin genes in
 RT Chironomus (Diptera)." Gene 251:153-163(2000);
 RL Gene 251:153-163(2000);
 DR EMBL: AF250305; AAF87714.1; -.
 FT NON_TER 1
 SQ SEQUENCE 23 AA; 233 MW; 3B0BF7A8FAB5E933 CRC64;

Query Match
 Best Local Similarity 20.0%; Score 25; DB 5; Length 23;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 RLLIAFSE 14
 Db 6 RIVGFYSE 13

RESULT 11

ID Q87081 PRELIMINARY; PRT; 23 AA.

AC Q87081;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE GLYCOPROTEIN C PRECURSOR (FRAGMENT).

GN GC.

OS Pseudorabies virus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TAXID=10345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BECKER;
 RX MEDLINE=96070924; PubMed=7499261;
 RA Ryan P., Edwards C.O.;
 RT "Systematic introduction of proline in a eukaryotic signal sequence
 suggests asymmetry within the hydrophobic core." J. Biol. Chem. 270:27876-27879(1995).
 DR EMBL: U29124; AAC54534.1; -.
 KW SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT NON_TER 23 23 MW; B7112B05ED406F3F CRC64;

SQ SEQUENCE 23 AA; 2229 MW; B7112B05ED406F3F CRC64;

RESULT 12

ID Q16061 PRELIMINARY; PRT; 24 AA.

AC Q16061;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE TNNT1 PROTEIN (FRAGMENT).

GN TNNT1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94006957; PubMed=8403232;

RA Novelli G., Gemarelli M., Sangiulio F., D'Agruma L., Lo Cicero S.,
 RA Melchionda S., DallaPiccola B.;
 RT "Isolation and cloning by a polymerase chain reaction of a genomic DNA
 fragment of the human slow skeletal tropomodulin (TNNT1) gene." Cell Biochemistry and Function 11:187-191(1993).

DR EMBL: S66057; AAD13978.1;
 DR EMBL: S66170; AAD13978.1; JOINED.
 DR EMBL: S66170; AAD13978.1;
 FT NON_TER 24 24 MW; 4A41B1A59FD34E5E CRC64;

SQ SEQUENCE 24 AA; 274 MW; 4A41B1A59FD34E5E CRC64;

Query Match
 Best Local Similarity 20.0%; Score 25; DB 4; Length 24;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 16 SHFSIUKGKA 24
 Db 6 SHAQKRKGKA 14

RESULT 13

ID P82833 PRELIMINARY; PRT; 24 AA.

AC P82833;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE BREVININ1BA.

OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OC NCBI_TaxID=30360;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE-2011700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -I- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC S AUREUS.
 CC -I- MASS SPECTROMETRY: MW=263; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Antibiotic.
 FT DISULFID 18 24 BY SIMILARITY.
 SQ SEQUENCE 24 AA; 2645 MW; CB524A45447DF4 CRC64;

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03; Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 CC DE
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 14

P82834 PRELIMINARY; PRT; 24 AA.

ID P82834; PRELIMINARY; PRT; 24 AA.

AC P82834; PRELIMINARY; PRT; 24 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE BREVININ-1BB.

OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OC NCBI_TaxID=30360;

RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE-2011700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -I- MASS SPECTROMETRY: MW=263; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Antibiotic.
 FT DISULFID 18 24 BY SIMILARITY.
 SQ SEQUENCE 24 AA; 2631 MW; CB524A454474CF4 CRC64;

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03; Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 CC DE
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 16

QBTR5 PRELIMINARY; PRT; 25 AA.

ID QBTR5
 AC QBTR5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE UNKNOWN (PROTEIN FOR IMAGE:3451138) (FRAGMENT).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OC NCBI_TaxID=9605;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CHORIOCARCINOMA;
 RA Strauberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003414; AAH03414; 1; -.

FT NON_TER 1 1
 SQ SEQUENCE 25 AA; 2825 MW; BB649418A85ABD5 CRC64;

Query Match 20.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 80.0%; Pred. No. 3.8e+03; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC DE
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 17

RA Mertelsmann R.; Herrmann F.; "Burkitt-like mutations in the c-myc gene locus in prolymphocytic RT leukemia"; Leukemia 8:897-902(1994); DR EMBL; S70386; AB30748.1; FT NON_TER 15 AA; 15 AA; 1772 MW; 883FB769FC6D5A98 CRC64;

Query Match 19.2%; Score 24; DB 4; Length 17; Best Local Similarity 36.4%; Pred. No. 3.7e+03; Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 IPLRLAFTSERH 15
ID :||| :||| :
AC 1 MPLNVNSFTSRN 11

RESULT 22
Q9UC55 PRELIMINARY; PRT; 16 AA.

ID Q9UC55
AC Q9UC55;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

RX PROTEIN C OSAKA 10 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93320735; PubMed=7763791;
RA Suzuki T.; Tagagi T.; Ohta S.;
RL Zool. Sci. 10:141-146(1993).
SEQUENCE 16 AA; 1875 MW; EBDP581FF3D325244 CRC64;

Query Match 19.2%; Score 24; DB 4; Length 16; Best Local Similarity 38.5%; Pred. No. 3.4e+03; Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 AETSESHFSIKR 22
ID :||| :||| :||| :
Db 4 SFLEELRHSSIER 16

RESULT 23
Q9BYF2 PRELIMINARY; PRT; 17 AA.

ID Q9BYF2
AC Q9BYF2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE RIBOSOMAL PROTEIN L39 (FRAGMENT).
GN RPL39.
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Uechi T.; Tanaka T.; Kenmochi N.; White K.C.; Babitt P.C.; Buchter D.D.; Kenyon G.L.; DE RIBOSOMAL PROTEIN L39 (FRAGMENT).
RN HSSP; P00563; ZORK 2425 MW; BFBC71D6D2A86E11 CRC64;
SQ SEQUENCE 20 AA; 2425 MW; BFBC71D6D2A86E11 CRC64;

Query Match 19.2%; Score 24; DB 13; Length 20; Best Local Similarity 40.0%; Pred. No. 4.3e+03; Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 FTSEHSFSL 20
ID :||| :||| :
Db 2 FGNTHNFRKL 11

Mon Jan 7 07:19:44 2002

us-09-441-061-2.closed.rspt

Page 8

Search completed: January 6, 2002, 09:56:29
Job time: 280 sec